SCORE Search Results Details for Application 10821669 and Search Result us-10-821-669-1_copy_673_691.szlm30.rapbn.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10821669 and Search Result us-10-821-669-1_copy_673_691.szlm30.rapbn.

start

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Search Report

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                          GenCore version 5.1.9
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:         November  1, 2006, 13:47:00 ; Search time 10.5556 Seconds
                                            (without alignments)
                                            150.742 Million cell updates/sec

Title:          US-10-821-669-1_COPY_673_691
Perfect score:  91
Sequence:       1 IPVLGTFALVSYIANKVLT 19

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       320231 seqs, 83745634 residues

Total number of hits satisfying chosen parameters:      64061

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :        Published_Applications_AA_New:*
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                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                7:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                8:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                    SUMMARIES

                  %
Result          Query
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RESULT 3
US-11-134-871-3348
; Sequence 3348, Application US/11134871
; Publication No. US20060141528A1
; GENERAL INFORMATION:
;  APPLICANT: Aebersold, Rudolf H.
;  APPLICANT:  Zhang, Hui
;  TITLE OF INVENTION: Compositions and Methods for
;  TITLE OF INVENTION:  Quatification of Serum Glycoproteins
;  FILE REFERENCE: 66661-116
;  CURRENT APPLICATION NUMBER: US/11/134,871
;  CURRENT FILING DATE:  2005-05-20
;  PRIOR APPLICATION NUMBER: 60/573,593
;  PRIOR FILING DATE: 2004-05-21
;  NUMBER OF SEQ ID NOS: 3602
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3348
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-134-871-3348

  Query Match             33.0%;  Score 30;  DB 7;  Length 19;
  Best Local Similarity   85.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FALVSYI 13
              ||||:||
Db          9 FALVNYI 15
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673-691

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RESULT 8
US-11-254-500-25
; Sequence 25, Application US/11254500
; Publication No. US20060147442A1
; GENERAL INFORMATION:
;  APPLICANT: Homan, Jane
;  APPLICANT:  Imboden, Michael D.
;  APPLICANT:  Riggs, Michael D.
;  APPLICANT:  Carryn, Stephane D.
;  TITLE OF INVENTION: Biocides
;  FILE REFERENCE: IOGEN-10173
;  CURRENT APPLICATION NUMBER: US/11/254,500
;  CURRENT FILING DATE:  2005-10-20
;  NUMBER OF SEQ ID NOS: 104
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Apis mellifera
US-11-254-500-25

  Query Match             30.8%;  Score 28;  DB 7;  Length 27;
  Best Local Similarity   50.0%;  Pred. No. 4.2e+02;
  Matches    6;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTFALVSYIANK 16
              |  ||:|:|: |
Db         12 GLPALISWISRK 23
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673-691

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RESULT 4
Q57012_STAAU
ID   Q57012_STAAU   PRELIMINARY;   PRT;    19 AA.
AC   Q57012;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 17.
DE   Peptide L.
OS   Staphylococcus aureus.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86135972; PubMed=3004956;
RA   Murphy E., Huwyler L., Do Carno de Freire Bastos M.;
RT   "Transposon Tn554: complete nucleotide sequence and isolation of
RT   transposition-defective and antibiotic-sensitive mutants.";
RL   EMBO J. 4:3357-3365(1985).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X03216; CAA26965.1; -; Genomic_DNA.
DR   InterPro; IPR013204; Leader_Erm.
SQ   SEQUENCE   19 AA;  2257 MW;  19F81AD99E4F2F9B CRC64;

  Query Match             34.1%;  Score 31;  DB 2;  Length 19;
  Best Local Similarity   42.9%;  Pred. No. 1.3e+03;
  Matches    6;  Conservative    5;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          4 LGTFALVSYIANKV 17
              :|||::  :: |||
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_715_733
Perfect score: 98
Sequence: 1 TNWLAKVNTQIDLIRKKMK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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2: geneseqp1990s:*
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4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	98	100.0	19	9	ADW11060	Adw11060 Clostridi
2	98	100.0	27	9	ADW11113	Adw11113 Clostridi
3	52	53.1	12	9	ADY20753	Ady20753 Botulinum
4	43	43.9	9	9	ADZ69803	Adz69803 Botulinum
5	38.5	39.3	22	2	AAY18841	Aay18841 Lecithin:
6	38.5	39.3	22	2	AAY19095	Aay19095 Lecithin:
7	38.5	39.3	22	2	AAY19349	Aay19349 Lecithin:
8	38.5	39.3	22	2	AAY18578	Aay18578 Lecithin:
9	38.5	39.3	22	8	ADG21058	Adg21058 Apolipopr
10	38.5	39.3	22	8	ADJ33000	Adj33000 Apo lipop
11	38	38.8	22	2	AAY18741	Aay18741 Lecithin:
12	38	38.8	22	2	AAY18995	Aay18995 Lecithin:

13	38	38.8	22	2	AAY19249	Aay19249 Lecithin:
14	38	38.8	22	2	AAY18478	Aay18478 Lecithin:
15	38	38.8	22	8	ADG20958	Adg20958 Apolipopr
16	38	38.8	22	8	ADJ32900	Adj32900 Apo lipop
17	36	36.7	22	2	AAR48545	Aar48545 Sequence
18	36	36.7	22	9	AEB28559	Aeb28559 Human apo
19	36	36.7	22	9	AEB11518	Aeb11518 Apolipopr
20	35	35.7	9	9	ADZ69802	Adz69802 Botulinum
21	35	35.7	14	9	ADY81602	Ady81602 HIV-1 ant
22	35	35.7	15	9	ADY81603	Ady81603 HIV-1 ant
23	35	35.7	16	9	ADY81604	Ady81604 HIV-1 ant
24	35	35.7	17	9	ADY81605	Ady81605 HIV-1 ant
25	35	35.7	27	6	ABP99874	Abp99874 Breast sp
26	35	35.7	27	8	ADF85937	Adf85937 Human bre
27	35	35.7	29	4	AAM33894	Aam33894 Peptide #
28	35	35.7	29	4	AAM73708	Aam73708 Human bon
29	35	35.7	29	4	AAM61013	Aam61013 Human bra
30	35	35.7	29	4	ABG55445	Abg55445 Human liv
31	35	35.7	29	5	ABG43583	Abg43583 Human pep
32	35	35.7	30	5	AAU79980	Aau79980 Human mal
33	34.5	35.2	27	5	AAE17354	Aae17354 Bovine vi
34	34.5	35.2	27	5	AAE17325	Aae17325 Recombina
35	34.5	35.2	27	5	AAE17327	Aae17327 Recombina
36	34.5	35.2	27	5	AAE17356	Aae17356 Border di
37	34.5	35.2	27	5	AAE17355	Aae17355 Bovine vi
38	34.5	35.2	27	5	AAE17326	Aae17326 Recombina
39	34	34.7	29	3	AAB23779	Aab23779 Entry vec
40	33.5	34.2	22	2	AAY18850	Aay18850 Lecithin:
41	33.5	34.2	22	2	AAY19104	Aay19104 Lecithin:
42	33.5	34.2	22	2	AAY19358	Aay19358 Lecithin:
43	33.5	34.2	22	2	AAY18587	Aay18587 Lecithin:
44	33.5	34.2	22	8	ADG21067	Adg21067 Apolipopr
45	33.5	34.2	22	8	ADJ33009	Adj33009 Apo lipop
46	33	33.7	9	8	ADK10588	Adk10588 Human pap
47	33	33.7	12	6	ABP68020	Abp68020 Bacillus
48	33	33.7	12	6	ABP68019	Abp68019 Bacillus
49	33	33.7	20	7	ADD36371	Add36371 Human THA
50	33	33.7	20	8	ADQ08994	Adq08994 Human THA
51	33	33.7	20	9	ADW46173	Adw46173 Human THA
52	33	33.7	22	2	AAY18785	Aay18785 Lecithin:
53	33	33.7	22	2	AAY18799	Aay18799 Lecithin:
54	33	33.7	22	2	AAY18754	Aay18754 Lecithin:
55	33	33.7	22	2	AAY19008	Aay19008 Lecithin:
56	33	33.7	22	2	AAY19053	Aay19053 Lecithin:
57	33	33.7	22	2	AAY19039	Aay19039 Lecithin:
58	33	33.7	22	2	AAY19262	Aay19262 Lecithin:
59	33	33.7	22	2	AAY19293	Aay19293 Lecithin:
60	33	33.7	22	2	AAY19307	Aay19307 Lecithin:
61	33	33.7	22	2	AAY18536	Aay18536 Lecithin:
62	33	33.7	22	2	AAY18522	Aay18522 Lecithin:
63	33	33.7	22	2	AAY18491	Aay18491 Lecithin:
64	33	33.7	22	8	ADG20971	Adg20971 Apolipopr
65	33	33.7	22	8	ADG21016	Adg21016 Apolipopr
66	33	33.7	22	8	ADG21002	Adg21002 Apolipopr
67	33	33.7	22	8	ADJ32913	Adj32913 Apo lipop
68	33	33.7	22	8	ADJ32944	Adj32944 Apo lipop
69	33	33.7	22	8	ADJ32958	Adj32958 Apo lipop
70	33	33.7	26	5	ABG66813	Abg66813 Human pro
71	32	32.7	11	6	ABP57646	Abp57646 Human CNI
72	32	32.7	14	2	AAR49341	Aar49341 P. falcip
73	32	32.7	14	2	AAW54723	Aaw54723 Peptide f

74	32	32.7	14	7	ADW33762	Adw33762 HLA bindi
75	32	32.7	14	7	ADW34995	Adw34995 HLA bindi
76	32	32.7	16	8	ADQ09109	Adq09109 THAP anti
77	32	32.7	21	5	AAU89228	Aau89228 Insulin/i
78	32	32.7	21	6	ADA04050	Ada04050 Insulin r
79	32	32.7	21	7	ADH95263	Adh95263 Insulin r
80	32	32.7	21	8	ADL67954	Adl67954 IGF-1R/IR
81	32	32.7	21	8	ADM37799	Adm37799 Anti-IR f
82	32	32.7	22	2	AAY18788	Aay18788 Lecithin:
83	32	32.7	22	2	AAY18801	Aay18801 Lecithin:
84	32	32.7	22	2	AAY18844	Aay18844 Lecithin:
85	32	32.7	22	2	AAY18743	Aay18743 Lecithin:
86	32	32.7	22	2	AAY19042	Aay19042 Lecithin:
87	32	32.7	22	2	AAY18997	Aay18997 Lecithin:
88	32	32.7	22	2	AAY19055	Aay19055 Lecithin:
89	32	32.7	22	2	AAY19098	Aay19098 Lecithin:
90	32	32.7	22	2	AAY19309	Aay19309 Lecithin:
91	32	32.7	22	2	AAY19251	Aay19251 Lecithin:
92	32	32.7	22	2	AAY19352	Aay19352 Lecithin:
93	32	32.7	22	2	AAY19296	Aay19296 Lecithin:
94	32	32.7	22	2	AAY18480	Aay18480 Lecithin:
95	32	32.7	22	2	AAY18538	Aay18538 Lecithin:
96	32	32.7	22	2	AAY18525	Aay18525 Lecithin:
97	32	32.7	22	2	AAY18581	Aay18581 Lecithin:
98	32	32.7	22	8	ADG21005	Adg21005 Apolipopr
99	32	32.7	22	8	ADG21061	Adg21061 Apolipopr
100	32	32.7	22	8	ADG21018	Adg21018 Apolipopr
101	32	32.7	22	8	ADG20960	Adg20960 Apolipopr
102	32	32.7	22	8	ADJ32902	Adj32902 Apo lipop
103	32	32.7	22	8	ADJ32947	Adj32947 Apo lipop
104	32	32.7	22	8	ADJ33003	Adj33003 Apo lipop
105	32	32.7	22	8	ADJ32960	Adj32960 Apo lipop
106	32	32.7	22	9	AEB09648	Aeb09648 Human apo
107	32	32.7	28	2	AAR73659	Aar73659 Ac-PDGF(2
108	32	32.7	28	2	AAR73658	Aar73658 PDGF(25-3
109	31.5	32.1	30	5	ABP29138	Abp29138 Streptoco
110	31	31.6	8	9	AEC13995	Aec13995 Enterococ
111	31	31.6	15	2	AAW73756	Aaw73756 M. tuberc
112	31	31.6	15	2	AAW73866	Aaw73866 M. tuberc
113	31	31.6	15	4	AAU08222	Aau08222 Mycobacte
114	31	31.6	15	4	AAB97804	Aab97804 gp100 der
115	31	31.6	15	4	AAB98194	Aab98194 Interfero
116	31	31.6	21	6	ABB82880	Abb82880 Dopamine
117	31	31.6	21	6	ABP58824	Abp58824 Melanoma-
118	31	31.6	22	2	AAW39966	Aaw39966 Peptide e
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120	31	31.6	22	2	AAY18810	Aay18810 Lecithin:
121	31	31.6	22	2	AAY18852	Aay18852 Lecithin:
122	31	31.6	22	2	AAY19106	Aay19106 Lecithin:
123	31	31.6	22	2	AAY19064	Aay19064 Lecithin:
124	31	31.6	22	2	AAY18974	Aay18974 Lecithin:
125	31	31.6	22	2	AAY19318	Aay19318 Lecithin:
126	31	31.6	22	2	AAY19228	Aay19228 Lecithin:
127	31	31.6	22	2	AAY19360	Aay19360 Lecithin:
128	31	31.6	22	2	AAY18457	Aay18457 Lecithin:
129	31	31.6	22	2	AAY18547	Aay18547 Lecithin:
130	31	31.6	22	2	AAY18589	Aay18589 Lecithin:
131	31	31.6	22	8	ADG20937	Adg20937 Apolipopr
132	31	31.6	22	8	ADG21027	Adg21027 Apolipopr
133	31	31.6	22	8	ADG21069	Adg21069 Apolipopr
134	31	31.6	22	8	ADJ33011	Adj33011 Apo lipop

135	31	31.6	22	8	ADJ32969	Adj32969 Apo lipop
136	31	31.6	22	8	ADJ32879	Adj32879 Apo lipop
137	31	31.6	23	8	ADM12473	Adm12473 Ii-key/gp
138	31	31.6	23	8	ADO38696	Ado38696 Melanocyt
139	31	31.6	24	10	AEF01181	Aef01181 Ii-key/ g
140	31	31.6	25	8	ABO54473	Abo54473 Human gen
141	31	31.6	30	5	AAU84859	Aau84859 Human gp1
142	31	31.6	30	7	ADG14992	Adg14992 Human SEC
143	30	30.6	10	5	AAU82796	Aau82796 Human Cal
144	30	30.6	10	9	ADW86252	Adw86252 Human cal
145	30	30.6	10	9	ADZ88977	Adz88977 Human cal
146	30	30.6	14	2	AAR81298	Aar81298 Anti-fung
147	30	30.6	14	2	AAR78128	Aar78128 Bacterial
148	30	30.6	14	2	AAR82368	Aar82368 BPI.264,
149	30	30.6	14	2	AAR87868	Aar87868 BPI.264 f
150	30	30.6	14	2	AAR76447	Aar76447 Bacterial
151	30	30.6	14	2	AAW06063	Aaw06063 Recombina
152	30	30.6	14	2	AAW04138	Aaw04138 Antifunga
153	30	30.6	14	2	AAW44503	Aaw44503 Anti-fung
154	30	30.6	14	2	AAW43689	Aaw43689 Bacterici
155	30	30.6	14	2	AAW63514	Aaw63514 Human BPI
156	30	30.6	14	2	AAY00480	Aay00480 Antifunga
157	30	30.6	14	3	AAB16254	Aab16254 Bacterici
158	30	30.6	14	4	AAB65404	Aab65404 Anti-fung
159	30	30.6	14	4	AAB52424	Aab52424 Peptide B
160	30	30.6	14	8	ADI66714	Adi66714 Rat bacte
161	30	30.6	14	8	ADM91446	Adm91446 Bacterici
162	30	30.6	15	2	AAW73755	Aaw73755 M. tuberc
163	30	30.6	15	2	AAW73865	Aaw73865 M. tuberc
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165	30	30.6	15	4	AAB86572	Aab86572 Human cyt
166	30	30.6	15	4	AAB19894	Aab19894 Neisseria
167	30	30.6	15	8	ADO77268	Ado77268 Human 213
168	30	30.6	15	9	ADW76239	Adw76239 Human cyt
169	30	30.6	15	9	AEC14055	Aec14055 Pseudomon
170	30	30.6	17	9	ADY38566	Ady38566 Antigenic
171	30	30.6	17	9	AED44638	Aed44638 Hs.516830
172	30	30.6	18	2	AAW18519	Aaw18519 RAC-PK pl
173	30	30.6	18	4	AAB77837	Aab77837 Core poly
174	30	30.6	18	10	AEF02100	Aef02100 Ii-key/ H
175	30	30.6	19	2	AAY18769	Aay18769 Lecithin:
176	30	30.6	19	2	AAY19023	Aay19023 Lecithin:
177	30	30.6	19	2	AAY19277	Aay19277 Lecithin:
178	30	30.6	19	2	AAY18506	Aay18506 Lecithin:
179	30	30.6	19	7	ADF14735	Adf14735 Diabetes
180	30	30.6	19	7	ADF14736	Adf14736 Diabetes
181	30	30.6	19	8	ADG20986	Adg20986 Apolipopr
182	30	30.6	19	8	ADJ32928	Adj32928 Apo lipop
183	30	30.6	19	9	ADW11059	Adw11059 Clostridi
184	30	30.6	20	2	AAY18761	Aay18761 Lecithin:
185	30	30.6	20	2	AAY19015	Aay19015 Lecithin:
186	30	30.6	20	2	AAY19269	Aay19269 Lecithin:
187	30	30.6	20	2	AAY18498	Aay18498 Lecithin:
188	30	30.6	20	3	AAY89436	Aay89436 Core poly
189	30	30.6	20	3	AAY96725	Aay96725 MADr3 C-t
190	30	30.6	20	4	ABB02319	Abb02319 Viral cor
191	30	30.6	20	4	ABB00844	Abb00844 Viral DP1
192	30	30.6	20	4	AAU13390	Aau13390 DP178-lik
193	30	30.6	20	5	ADE02339	Ade02339 Hybrid po
194	30	30.6	20	8	ADG20978	Adg20978 Apolipopr
195	30	30.6	20	8	ADJ32920	Adj32920 Apo lipop

196	30	30.6	21	2	AAY18744	Aay18744 Lecithin:
197	30	30.6	21	2	AAY18998	Aay18998 Lecithin:
198	30	30.6	21	2	AAY19252	Aay19252 Lecithin:
199	30	30.6	21	2	AAY18481	Aay18481 Lecithin:
200	30	30.6	21	8	ADG20961	Adg20961 Apolipopr
201	30	30.6	21	8	ADJ32903	Adj32903 Apo lipop
202	30	30.6	22	2	AAY18742	Aay18742 Lecithin:
203	30	30.6	22	2	AAY18731	Aay18731 Lecithin:
204	30	30.6	22	2	AAY18796	Aay18796 Lecithin:
205	30	30.6	22	2	AAY18773	Aay18773 Lecithin:
206	30	30.6	22	2	AAY18757	Aay18757 Lecithin:
207	30	30.6	22	2	AAY18795	Aay18795 Lecithin:
208	30	30.6	22	2	AAY18723	Aay18723 Lecithin:
209	30	30.6	22	2	AAY18724	Aay18724 Lecithin:
210	30	30.6	22	2	AAY18725	Aay18725 Lecithin:
211	30	30.6	22	2	AAY18753	Aay18753 Lecithin:
212	30	30.6	22	2	AAY18798	Aay18798 Lecithin:
213	30	30.6	22	2	AAY18794	Aay18794 Lecithin:
214	30	30.6	22	2	AAY18740	Aay18740 Lecithin:
215	30	30.6	22	2	AAY18792	Aay18792 Lecithin:
216	30	30.6	22	2	AAY18748	Aay18748 Lecithin:
217	30	30.6	22	2	AAY18752	Aay18752 Lecithin:
218	30	30.6	22	2	AAY18756	Aay18756 Lecithin:
219	30	30.6	22	2	AAY19052	Aay19052 Lecithin:
220	30	30.6	22	2	AAY18977	Aay18977 Lecithin:
221	30	30.6	22	2	AAY19027	Aay19027 Lecithin:
222	30	30.6	22	2	AAY18978	Aay18978 Lecithin:
223	30	30.6	22	2	AAY19007	Aay19007 Lecithin:
224	30	30.6	22	2	AAY19049	Aay19049 Lecithin:
225	30	30.6	22	2	AAY18996	Aay18996 Lecithin:
226	30	30.6	22	2	AAY19006	Aay19006 Lecithin:
227	30	30.6	22	2	AAY19011	Aay19011 Lecithin:
228	30	30.6	22	2	AAY19002	Aay19002 Lecithin:
229	30	30.6	22	2	AAY19050	Aay19050 Lecithin:
230	30	30.6	22	2	AAY18985	Aay18985 Lecithin:
231	30	30.6	22	2	AAY19010	Aay19010 Lecithin:
232	30	30.6	22	2	AAY19046	Aay19046 Lecithin:
233	30	30.6	22	2	AAY18979	Aay18979 Lecithin:
234	30	30.6	22	2	AAY18994	Aay18994 Lecithin:
235	30	30.6	22	2	AAY19048	Aay19048 Lecithin:
236	30	30.6	22	2	AAY19256	Aay19256 Lecithin:
237	30	30.6	22	2	AAY19302	Aay19302 Lecithin:
238	30	30.6	22	2	AAY19260	Aay19260 Lecithin:
239	30	30.6	22	2	AAY19281	Aay19281 Lecithin:
240	30	30.6	22	2	AAY19233	Aay19233 Lecithin:
241	30	30.6	22	2	AAY19304	Aay19304 Lecithin:
242	30	30.6	22	2	AAY19232	Aay19232 Lecithin:
243	30	30.6	22	2	AAY19261	Aay19261 Lecithin:
244	30	30.6	22	2	AAY19265	Aay19265 Lecithin:
245	30	30.6	22	2	AAY19300	Aay19300 Lecithin:
246	30	30.6	22	2	AAY19264	Aay19264 Lecithin:
247	30	30.6	22	2	AAY19231	Aay19231 Lecithin:
248	30	30.6	22	2	AAY19306	Aay19306 Lecithin:
249	30	30.6	22	2	AAY19239	Aay19239 Lecithin:
250	30	30.6	22	2	AAY19248	Aay19248 Lecithin:
251	30	30.6	22	2	AAY19250	Aay19250 Lecithin:
252	30	30.6	22	2	AAY19303	Aay19303 Lecithin:
253	30	30.6	22	2	AAY18533	Aay18533 Lecithin:
254	30	30.6	22	2	AAY18529	Aay18529 Lecithin:
255	30	30.6	22	2	AAY18494	Aay18494 Lecithin:
256	30	30.6	22	2	AAY18489	Aay18489 Lecithin:

257	30	30.6	22	2	AAY18479	Aay18479 Lecithin:
258	30	30.6	22	2	AAY18490	Aay18490 Lecithin:
259	30	30.6	22	2	AAY18535	Aay18535 Lecithin:
260	30	30.6	22	2	AAY18493	Aay18493 Lecithin:
261	30	30.6	22	2	AAY18510	Aay18510 Lecithin:
262	30	30.6	22	2	AAY18460	Aay18460 Lecithin:
263	30	30.6	22	2	AAY18461	Aay18461 Lecithin:
264	30	30.6	22	2	AAY18531	Aay18531 Lecithin:
265	30	30.6	22	2	AAY18532	Aay18532 Lecithin:
266	30	30.6	22	2	AAY18485	Aay18485 Lecithin:
267	30	30.6	22	2	AAY18462	Aay18462 Lecithin:
268	30	30.6	22	2	AAY18468	Aay18468 Lecithin:
269	30	30.6	22	2	AAY18477	Aay18477 Lecithin:
270	30	30.6	22	8	ADG20948	Adg20948 Apolipopr
271	30	30.6	22	8	ADG20965	Adg20965 Apolipopr
272	30	30.6	22	8	ADG20969	Adg20969 Apolipopr
273	30	30.6	22	8	ADG20942	Adg20942 Apolipopr
274	30	30.6	22	8	ADG20973	Adg20973 Apolipopr
275	30	30.6	22	8	ADG21009	Adg21009 Apolipopr
276	30	30.6	22	8	ADG20941	Adg20941 Apolipopr
277	30	30.6	22	8	ADG20974	Adg20974 Apolipopr
278	30	30.6	22	8	ADG21012	Adg21012 Apolipopr
279	30	30.6	22	8	ADG21015	Adg21015 Apolipopr
280	30	30.6	22	8	ADG20959	Adg20959 Apolipopr
281	30	30.6	22	8	ADG21011	Adg21011 Apolipopr
282	30	30.6	22	8	ADG20970	Adg20970 Apolipopr
283	30	30.6	22	8	ADG20940	Adg20940 Apolipopr
284	30	30.6	22	8	ADG20957	Adg20957 Apolipopr
285	30	30.6	22	8	ADG20990	Adg20990 Apolipopr
286	30	30.6	22	8	ADG21013	Adg21013 Apolipopr
287	30	30.6	22	8	ADJ32955	Adj32955 Apo lipop
288	30	30.6	22	8	ADJ32884	Adj32884 Apo lipop
289	30	30.6	22	8	ADJ32953	Adj32953 Apo lipop
290	30	30.6	22	8	ADJ32899	Adj32899 Apo lipop
291	30	30.6	22	8	ADJ32890	Adj32890 Apo lipop
292	30	30.6	22	8	ADJ32882	Adj32882 Apo lipop
293	30	30.6	22	8	ADJ32907	Adj32907 Apo lipop
294	30	30.6	22	8	ADJ32883	Adj32883 Apo lipop
295	30	30.6	22	8	ADJ32951	Adj32951 Apo lipop
296	30	30.6	22	8	ADJ32911	Adj32911 Apo lipop
297	30	30.6	22	8	ADJ32901	Adj32901 Apo lipop
298	30	30.6	22	8	ADJ32916	Adj32916 Apo lipop
299	30	30.6	22	8	ADJ32912	Adj32912 Apo lipop
300	30	30.6	22	8	ADJ32954	Adj32954 Apo lipop
301	30	30.6	22	8	ADJ32915	Adj32915 Apo lipop
302	30	30.6	22	8	ADJ32932	Adj32932 Apo lipop
303	30	30.6	22	8	ADJ32957	Adj32957 Apo lipop
304	30	30.6	24	10	AEE38455	Aee38455 Human ser
305	30	30.6	25	2	AAR36467	Aar36467 DFI-22.2(
306	30	30.6	25	2	AAR51815	Aar51815 Der f I d
307	30	30.6	25	2	AAR77119	Aar77119 Dermatoph
308	30	30.6	25	2	AAW71898	Aaw71898 Dermatoph
309	30	30.6	25	2	AAY50444	Aay50444 Dermatoph
310	30	30.6	25	4	AAU19047	Aau19047 T-cell ep
311	30	30.6	25	6	ABP97152	Abp97152 Smad3C fr
312	30	30.6	25	6	ABP97153	Abp97153 Smad3C fr
313	30	30.6	27	3	AAB29253	Aab29253 Mouse cyc
314	30	30.6	27	3	AAY43808	Aay43808 Cyclin de
315	30	30.6	27	4	AAB62207	Aab62207 Mouse cyc
316	30	30.6	27	4	AAB67682	Aab67682 Cyclin de
317	30	30.6	27	4	AAM52559	Aam52559 Murine cy

318	30	30.6	27	4	AAB74488	Aab74488 Murine cy
319	30	30.6	27	4	AAB82393	Aab82393 Mouse cyc
320	30	30.6	27	4	AAB74462	Aab74462 Murine cy
321	30	30.6	27	4	AAG62584	Aag62584 Murine cy
322	30	30.6	27	4	AAB84850	Aab84850 Murine cy
323	30	30.6	27	4	AAE09727	Aae09727 Destructi
324	30	30.6	27	6	ABR39541	Abr39541 Mouse cyc
325	30	30.6	27	6	ABG73727	Abg73727 Murine cy
326	30	30.6	27	6	ADA07077	Ada07077 Mouse cyc
327	30	30.6	27	7	ADF90359	Adf90359 Mouse Cyc
328	30	30.6	27	7	ADH69411	Adh69411 Mouse cyc
329	30	30.6	27	8	ADO26208	Ado26208 Mouse cyc
330	30	30.6	27	9	ADY97775	Ady97775 Mouse cyc
331	30	30.6	29	2	AAR36466	Aar36466 DFI-22.1(
332	30	30.6	29	2	AAR36468	Aar36468 DFI-22.4(
333	30	30.6	29	2	AAR51814	Aar51814 Der f I d
334	30	30.6	29	2	AAR51816	Aar51816 Der f I d
335	30	30.6	29	2	AAW71990	Aaw71990 Dermatoph
336	30	30.6	29	2	AAW71989	Aaw71989 Dermatoph
337	30	30.6	29	2	AAY50445	Aay50445 Dermatoph
338	30	30.6	29	2	AAY50443	Aay50443 Dermatoph
339	30	30.6	29	4	AAU19048	Aau19048 T-cell ep
340	30	30.6	29	4	AAU19046	Aau19046 T-cell ep
341	30	30.6	29	4	AAE05049	Aae05049 Human ZCY
342	30	30.6	29	7	ABR83686	Abr83686 Human IL-
343	30	30.6	29	7	ADH69550	Adh69550 Human ZCY
344	30	30.6	29	10	AEE36210	Aee36210 Human ser
345	29	29.6	8	5	ABP53199	Abp53199 Zinc fing
346	29	29.6	8	6	ABU60745	Abu60745 Phage dis
347	29	29.6	8	7	ADJ98398	Adj98398 Zinc fing
348	29	29.6	13	6	ABR62229	Abr62229 Apolipopr
349	29	29.6	14	2	AAR81162	Aar81162 Anti-fung
350	29	29.6	14	2	AAR77991	Aar77991 BPI prote
351	29	29.6	14	2	AAR86531	Aar86531 BPI.83 fo
352	29	29.6	14	2	AAR76318	Aar76318 Bacterial
353	29	29.6	14	2	AAW05928	Aaw05928 Recombina
354	29	29.6	14	2	AAW63379	Aaw63379 Human BPI
355	29	29.6	14	3	AAB16117	Aab16117 Bacterici
356	29	29.6	14	4	AAB52287	Aab52287 Peptide B
357	29	29.6	14	8	ADH68260	Adh68260 GPCR rela
358	29	29.6	14	8	ADI66579	Adi66579 Rat bacte
359	29	29.6	15	5	ABP56527	Abp56527 Human P24
360	29	29.6	15	6	ABR57623	Abr57623 Human end
361	29	29.6	15	6	ABB98946	Abb98946 Translati
362	29	29.6	16	2	AAW47956	Aaw47956 AE110 ext
363	29	29.6	19	4	ABB43395	Abb43395 Peptide #
364	29	29.6	19	4	AAM37276	Aam37276 Peptide #
365	29	29.6	19	4	AAM77147	Aam77147 Human bon
366	29	29.6	19	4	AAM64319	Aam64319 Human bra
367	29	29.6	19	4	ABG58772	Abg58772 Human liv
368	29	29.6	19	5	ABG46158	Abg46158 Human pep
369	29	29.6	22	2	AAY18712	Aay18712 Lecithin:
370	29	29.6	22	2	AAY18787	Aay18787 Lecithin:
371	29	29.6	22	2	AAY18855	Aay18855 Lecithin:
372	29	29.6	22	2	AAY18806	Aay18806 Lecithin:
373	29	29.6	22	2	AAY18705	Aay18705 Lecithin:
374	29	29.6	22	2	AAY18793	Aay18793 Lecithin:
375	29	29.6	22	2	AAY18760	Aay18760 Lecithin:
376	29	29.6	22	2	AAY18763	Aay18763 Lecithin:
377	29	29.6	22	2	AAY19014	Aay19014 Lecithin:
378	29	29.6	22	2	AAY19109	Aay19109 Lecithin:

379	29	29.6	22	2	AAY19041	Aay19041 Lecithin:
380	29	29.6	22	2	AAY18966	Aay18966 Lecithin:
381	29	29.6	22	2	AAY18959	Aay18959 Lecithin:
382	29	29.6	22	2	AAY19047	Aay19047 Lecithin:
383	29	29.6	22	2	AAY19017	Aay19017 Lecithin:
384	29	29.6	22	2	AAY19060	Aay19060 Lecithin:
385	29	29.6	22	2	AAY19213	Aay19213 Lecithin:
386	29	29.6	22	2	AAY19268	Aay19268 Lecithin:
387	29	29.6	22	2	AAY19271	Aay19271 Lecithin:
388	29	29.6	22	2	AAY19314	Aay19314 Lecithin:
389	29	29.6	22	2	AAY19363	Aay19363 Lecithin:
390	29	29.6	22	2	AAY19220	Aay19220 Lecithin:
391	29	29.6	22	2	AAY19295	Aay19295 Lecithin:
392	29	29.6	22	2	AAY19301	Aay19301 Lecithin:
393	29	29.6	22	2	AAY18524	Aay18524 Lecithin:
394	29	29.6	22	2	AAY18500	Aay18500 Lecithin:
395	29	29.6	22	2	AAY18449	Aay18449 Lecithin:
396	29	29.6	22	2	AAY18530	Aay18530 Lecithin:
397	29	29.6	22	2	AAY18543	Aay18543 Lecithin:
398	29	29.6	22	2	AAY18592	Aay18592 Lecithin:
399	29	29.6	22	2	AAY18442	Aay18442 Lecithin:
400	29	29.6	22	2	AAY18497	Aay18497 Lecithin:
401	29	29.6	22	8	ADG21072	Adg21072 Apolipopr
402	29	29.6	22	8	ADG20929	Adg20929 Apolipopr
403	29	29.6	22	8	ADG21023	Adg21023 Apolipopr
404	29	29.6	22	8	ADG21004	Adg21004 Apolipopr
405	29	29.6	22	8	ADG20977	Adg20977 Apolipopr
406	29	29.6	22	8	ADG20922	Adg20922 Apolipopr
407	29	29.6	22	8	ADG21010	Adg21010 Apolipopr
408	29	29.6	22	8	ADG20980	Adg20980 Apolipopr
409	29	29.6	22	8	ADJ32946	Adj32946 Apo lipop
410	29	29.6	22	8	ADJ32919	Adj32919 Apo lipop
411	29	29.6	22	8	ADJ32965	Adj32965 Apo lipop
412	29	29.6	22	8	ADJ32871	Adj32871 Apo lipop
413	29	29.6	22	8	ADJ32864	Adj32864 Apo lipop
414	29	29.6	22	8	ADJ32922	Adj32922 Apo lipop
415	29	29.6	22	8	ADJ32952	Adj32952 Apo lipop
416	29	29.6	22	8	ADJ33014	Adj33014 Apo lipop
417	29	29.6	22	8	ADT39374	Adt39374 hSARS vir
418	29	29.6	22	8	ADS78794	Ads78794 SARS viru
419	29	29.6	22	8	ADT36904	Adt36904 hSARS vir
420	29	29.6	23	7	ADL33660	Adl33660 Mutated z
421	29	29.6	23	7	ADL33631	Adl33631 Mutated z
422	29	29.6	24	2	AAY21285	Aay21285 Human sem
423	29	29.6	24	4	AAB81887	Aab81887 Nerve cel
424	29	29.6	24	9	ADV99788	Adv99788 Glucanase
425	29	29.6	25	10	AEE37290	Aee37290 Human ser
426	29	29.6	26	4	ABB37713	Abb37713 Peptide #
427	29	29.6	28	4	AAM21751	Aam21751 Peptide #
428	29	29.6	28	4	ABB44120	Abb44120 Peptide #
429	29	29.6	28	4	AAM38067	Aam38067 Peptide #
430	29	29.6	28	4	ABB27007	Abb27007 Protein #
431	29	29.6	28	4	AAM77847	Aam77847 Human bon
432	29	29.6	28	4	AAM65142	Aam65142 Human bra
433	29	29.6	28	4	ABG59502	Abg59502 Human liv
434	29	29.6	28	8	ADG71882	Adg71882 Human NOV
435	29	29.6	28	8	ADJ87219	Adj87219 Human G p
436	29	29.6	28	10	AEE28018	Aee28018 S. pneumo
437	29	29.6	28	10	AEE28072	Aee28072 H, influe
438	29	29.6	28	10	AEF10501	Aef10501 Human NOV
439	29	29.6	29	7	ABW00978	Abw00978 Mutant Ja

440	29	29.6	29	7	ADE86421	Ade86421 Mutant JA
441	29	29.6	30	5	AAU84858	Aau84858 Human gp1
442	28.5	29.1	22	2	AAY18848	Aay18848 Lecithin:
443	28.5	29.1	22	2	AAY18845	Aay18845 Lecithin:
444	28.5	29.1	22	2	AAY18862	Aay18862 Lecithin:
445	28.5	29.1	22	2	AAY19099	Aay19099 Lecithin:
446	28.5	29.1	22	2	AAY19102	Aay19102 Lecithin:
447	28.5	29.1	22	2	AAY19116	Aay19116 Lecithin:
448	28.5	29.1	22	2	AAY19353	Aay19353 Lecithin:
449	28.5	29.1	22	2	AAY19370	Aay19370 Lecithin:
450	28.5	29.1	22	2	AAY19356	Aay19356 Lecithin:
451	28.5	29.1	22	2	AAY18599	Aay18599 Lecithin:
452	28.5	29.1	22	2	AAY18585	Aay18585 Lecithin:
453	28.5	29.1	22	2	AAY18582	Aay18582 Lecithin:
454	28.5	29.1	22	8	ADG21079	Adg21079 Apolipopr
455	28.5	29.1	22	8	ADG21065	Adg21065 Apolipopr
456	28.5	29.1	22	8	ADG21062	Adg21062 Apolipopr
457	28.5	29.1	22	8	ADJ33004	Adj33004 Apo lipop
458	28.5	29.1	22	8	ADJ33007	Adj33007 Apo lipop
459	28.5	29.1	22	8	ADJ33021	Adj33021 Apo lipop
460	28.5	29.1	25	2	AAR73663	Aar73663 Ac-PDGF(2
461	28	28.6	7	4	ABB56099	Abb56099 Vascular
462	28	28.6	7	4	AAU28516	Aau28516 DPI trypt
463	28	28.6	7	4	AAU24833	Aau24833 Schizophr
464	28	28.6	7	4	AAU26162	Aau26162 Depressio
465	28	28.6	7	4	AAU15177	Aau15177 Schizophr
466	28	28.6	7	4	ABB52072	Abb52072 Human API
467	28	28.6	7	5	ABG78630	Abg78630 Multiple
468	28	28.6	7	6	ABR58923	Abr58923 Alzheimer
469	28	28.6	7	8	ADN32135	Adn32135 Human Alz
470	28	28.6	7	8	ADO78444	Ado78444 Schizophr
471	28	28.6	8	8	ADK10579	Adk10579 Human pap
472	28	28.6	10	4	AAG87262	Aag87262 Saccharom
473	28	28.6	10	8	ADK10596	Adk10596 Human pap
474	28	28.6	12	9	ADY81626	Ady81626 HIV-1 ant
475	28	28.6	12	9	ADY81627	Ady81627 HIV-1 ant
476	28	28.6	13	3	AAY88906	Aay88906 Core poly
477	28	28.6	13	4	AAB77261	Aab77261 Core poly
478	28	28.6	13	4	ABB00265	Abb00265 Viral DP1
479	28	28.6	13	4	ABB01739	Abb01739 Viral cor
480	28	28.6	13	4	AAU12814	Aau12814 DP178-lik
481	28	28.6	13	5	ADE01759	Ade01759 Hybrid po
482	28	28.6	13	6	ABO10308	Abo10308 HPIV3 F1
483	28	28.6	13	6	ABP68027	Abp68027 Bacillus
484	28	28.6	13	9	ADY81628	Ady81628 HIV-1 ant
485	28	28.6	13	9	AEA24073	Aea24073 Human pro
486	28	28.6	14	2	AAW22990	Aaw22990 Human ser
487	28	28.6	14	9	ADY81646	Ady81646 HIV-1 ant
488	28	28.6	14	9	ADY81598	Ady81598 HIV-1 ant
489	28	28.6	14	9	ADY81629	Ady81629 HIV-1 ant
490	28	28.6	15	4	ABR52288	Abr52288 IgE-react
491	28	28.6	15	4	ABR51487	Abr51487 Pen a 1 I
492	28	28.6	15	4	ABR51339	Abr51339 Shrimp Pe
493	28	28.6	15	8	ADO77295	Ado77295 Human 213
494	28	28.6	15	8	ADO77183	Ado77183 Human 213
495	28	28.6	15	8	ADO77189	Ado77189 Human 213
496	28	28.6	15	8	ADO77269	Ado77269 Human 213
497	28	28.6	15	8	ADP26474	Adp26474 Plasmodiu
498	28	28.6	15	9	ADV21748	Adv21748 SIV pol p
499	28	28.6	15	9	ADY81631	Ady81631 HIV-1 ant
500	28	28.6	15	9	ADY81599	Ady81599 HIV-1 ant

501	28	28.6	15	9	ADY81647	Ady81647 HIV-1 ant
502	28	28.6	15	9	ADY81630	Ady81630 HIV-1 ant
503	28	28.6	15	9	ADY81648	Ady81648 HIV-1 ant
504	28	28.6	16	2	AAW70134	Aaw70134 Peptide p
505	28	28.6	16	4	AAE05591	Aae05591 N-termina
506	28	28.6	16	6	ABO43454	Abo43454 M. tuberc
507	28	28.6	16	9	ADY81600	Ady81600 HIV-1 ant
508	28	28.6	16	9	ADY81649	Ady81649 HIV-1 ant
509	28	28.6	16	9	ADY81632	Ady81632 HIV-1 ant
510	28	28.6	17	9	ADY81601	Ady81601 HIV-1 ant
511	28	28.6	18	3	AAB00146	Aab00146 Human pro
512	28	28.6	18	5	ABG31672	Abg31672 Vitamin K
513	28	28.6	18	8	ADI28365	Adi28365 Human TIE
514	28	28.6	18	9	ADV67399	Adv67399 Amino aci
515	28	28.6	19	7	ADC98804	Adc98804 Streptoco
516	28	28.6	19	7	ADF14672	Adf14672 Rheumatoi
517	28	28.6	19	9	AED27832	Aed27832 Guanylate
518	28	28.6	20	2	AAW33933	Aaw33933 D2 dopami
519	28	28.6	20	4	ABB36881	Abb36881 Peptide #
520	28	28.6	20	4	AAM70031	Aam70031 Human bon
521	28	28.6	20	4	AAM57628	Aam57628 Human bra
522	28	28.6	20	4	AAM05511	Aam05511 Peptide #
523	28	28.6	20	5	ABG39662	Abg39662 Human pep
524	28	28.6	20	6	ABP55288	Abp55288 Human adr
525	28	28.6	20	6	ABP55287	Abp55287 Human dop
526	28	28.6	20	8	ABO58184	Abo58184 Human gen
527	28	28.6	20	9	ADW52426	Adw52426 Human PL
528	28	28.6	21	2	AAR36449	Aar36449 DFI-4(40-
529	28	28.6	21	2	AAR51797	Aar51797 Der f I d
530	28	28.6	21	2	AAW71972	Aaw71972 Dermatoph
531	28	28.6	21	2	AAY50426	Aay50426 Dermatoph
532	28	28.6	21	4	AAU19029	Aau19029 T-cell ep
533	28	28.6	21	5	ABG60820	Abg60820 Cellular
534	28	28.6	21	6	ABB82879	Abb82879 Dopamine
535	28	28.6	21	8	ADT39739	Adt39739 hSARS vir
536	28	28.6	21	8	ADS79158	Ads79158 SARS viru
537	28	28.6	21	8	ADT37269	Adt37269 hSARS vir
538	28	28.6	21	8	ABY03652	Aby03652 SARS coro
539	28	28.6	21	9	ADY62294	Ady62294 Human RHA
540	28	28.6	21	9	ADY96582	Ady96582 RHAMM rel
541	28	28.6	21	9	ADZ11922	Adz11922 Human RHA
542	28	28.6	22	2	AAY18782	Aay18782 Lecithin:
543	28	28.6	22	2	AAY18777	Aay18777 Lecithin:
544	28	28.6	22	2	AAY18800	Aay18800 Lecithin:
545	28	28.6	22	2	AAY18797	Aay18797 Lecithin:
546	28	28.6	22	2	AAY19031	Aay19031 Lecithin:
547	28	28.6	22	2	AAY19054	Aay19054 Lecithin:
548	28	28.6	22	2	AAY19051	Aay19051 Lecithin:
549	28	28.6	22	2	AAY19036	Aay19036 Lecithin:
550	28	28.6	22	2	AAY19290	Aay19290 Lecithin:
551	28	28.6	22	2	AAY19285	Aay19285 Lecithin:
552	28	28.6	22	2	AAY19308	Aay19308 Lecithin:
553	28	28.6	22	2	AAY19305	Aay19305 Lecithin:
554	28	28.6	22	2	AAY18514	Aay18514 Lecithin:
555	28	28.6	22	2	AAY18519	Aay18519 Lecithin:
556	28	28.6	22	2	AAY18537	Aay18537 Lecithin:
557	28	28.6	22	2	AAY18534	Aay18534 Lecithin:
558	28	28.6	22	8	ADG20994	Adg20994 Apolipopr
559	28	28.6	22	8	ADG21014	Adg21014 Apolipopr
560	28	28.6	22	8	ADG20999	Adg20999 Apolipopr
561	28	28.6	22	8	ADG21017	Adg21017 Apolipopr

562	28	28.6	22	8	ADJ32956	Adj32956 Apo lipop
563	28	28.6	22	8	ADJ32936	Adj32936 Apo lipop
564	28	28.6	22	8	ADJ32959	Adj32959 Apo lipop
565	28	28.6	22	8	ADJ32941	Adj32941 Apo lipop
566	28	28.6	22	10	AEE91990	Aee91990 Polynucle
567	28	28.6	23	2	AAR50814	Aar50814 G-protein
568	28	28.6	23	2	AAR89195	Aar89195 GPR adren
569	28	28.6	23	2	AAW02746	Aaw02746 G-protein
570	28	28.6	24	2	AAW33926	Aaw33926 D2 dopami
571	28	28.6	24	2	AAW39994	Aaw39994 Peptide e
572	28	28.6	25	2	AAW40243	Aaw40243 H. pylori
573	28	28.6	25	2	AAY27802	Aay27802 Human sec
574	28	28.6	25	6	ABB82545	Abb82545 Transport
575	28	28.6	25	6	ABO14294	Abo14294 Novel hum
576	28	28.6	25	8	ADG78702	Adg78702 Human sec
577	28	28.6	25	8	ADN60992	Adn60992 Human sec
578	28	28.6	26	4	AAO04818	Aao04818 Human pol
579	28	28.6	28	10	AEE28038	Aee28038 S.aureus
580	28	28.6	29	3	AAY89018	Aay89018 Core poly
581	28	28.6	29	3	AAB08357	Aab08357 Amino aci
582	28	28.6	29	4	AAB77373	Aab77373 Core poly
583	28	28.6	29	4	ABB01851	Abb01851 Viral cor
584	28	28.6	29	4	ABB00377	Abb00377 Viral DP1
585	28	28.6	29	4	AAU12926	Aau12926 DP178-lik
586	28	28.6	29	5	ADE01871	Ade01871 Hybrid po
587	28	28.6	29	6	ABO10310	Abo10310 HPIV3 F1
588	28	28.6	30	3	AAY99896	Aay99896 Peptide e
589	28	28.6	30	5	AAM49591	Aam49591 Human bet
590	27.5	28.1	20	8	ADU20811	Adu20811 Random st
591	27.5	28.1	26	4	AAM77099	Aam77099 Human bon
592	27.5	28.1	26	4	ABG58743	Abg58743 Human liv
593	27.5	28.1	30	2	AAR60067	Aar60067 Antimicro
594	27	27.6	9	2	AAR73669	Aar73669 Labelled
595	27	27.6	9	2	AAR73652	Aar73652 Ac-PDGF(7
596	27	27.6	9	2	AAR73651	Aar73651 PDGF(73-8
597	27	27.6	9	4	AAB75780	Aab75780 HLA class
598	27	27.6	10	2	AAR73653	Aar73653 PDGF(73-8
599	27	27.6	10	2	AAR73670	Aar73670 Labelled
600	27	27.6	10	2	AAR73654	Aar73654 Ac-PDGF(7
601	27	27.6	10	2	AAW76008	Aaw76008 LM609 gra
602	27	27.6	10	4	AAB75788	Aab75788 HLA class
603	27	27.6	10	4	AAB61366	Aab61366 LM609 VH
604	27	27.6	10	6	ABO19804	Abo19804 LM609 hea
605	27	27.6	10	7	ADG71810	Adg71810 Modified
606	27	27.6	10	8	ADJ57991	Adj57991 Murine LM
607	27	27.6	10	8	ABY01363	Aby01363 SARS coro
608	27	27.6	10	8	ABY01202	Aby01202 SARS coro
609	27	27.6	11	4	AAU28745	Aau28745 DPI trypt
610	27	27.6	11	4	AAU26393	Aau26393 Depressio
611	27	27.6	11	4	ABB52317	Abb52317 Human API
612	27	27.6	11	4	ABB52301	Abb52301 Human API
613	27	27.6	11	4	ABB52371	Abb52371 Human API
614	27	27.6	11	4	ABB52409	Abb52409 Human API
615	27	27.6	11	6	ABP57132	Abp57132 Breast ca
616	27	27.6	11	6	ABR58785	Abr58785 Alzheimer
617	27	27.6	11	8	ADN32058	Adn32058 Human Alz
618	27	27.6	11	9	AEA45350	Aea45350 Apolipopr
619	27	27.6	11	10	AEF40671	Aef40671 Pregnancy
620	27	27.6	12	8	ADO06896	Ado06896 Porcine r
621	27	27.6	13	4	AAU04993	Aau04993 N-termina
622	27	27.6	13	5	AAU86053	Aau86053 Human glu

623	27	27.6	13	6	ABP68026	Abp68026 Bacillus
624	27	27.6	13	6	ABP68023	Abp68023 Bacillus
625	27	27.6	13	6	ABP68021	Abp68021 Bacillus
626	27	27.6	13	6	ABP68022	Abp68022 Bacillus
627	27	27.6	13	6	ADA43078	Ada43078 HLA-DR be
628	27	27.6	13	10	AEF02148	Aef02148 Ii-key hy
629	27	27.6	14	2	AAR63742	Aar63742 BPI deriv
630	27	27.6	14	2	AAR61414	Aar61414 PDGF-B re
631	27	27.6	14	2	AAR81303	Aar81303 Anti-fung
632	27	27.6	14	2	AAR81302	Aar81302 Anti-fung
633	27	27.6	14	2	AAR81119	Aar81119 Anti-fung
634	27	27.6	14	2	AAR78132	Aar78132 Bacterial
635	27	27.6	14	2	AAR78133	Aar78133 Bacterial
636	27	27.6	14	2	AAR75995	Aar75995 BPI prote
637	27	27.6	14	2	AAR82373	Aar82373 BPI.269,
638	27	27.6	14	2	AAR82372	Aar82372 BPI.268,
639	27	27.6	14	2	AAR87872	Aar87872 BPI.268 f
640	27	27.6	14	2	AAR86489	Aar86489 BPI.32 fo
641	27	27.6	14	2	AAR87873	Aar87873 BPI.269 f
642	27	27.6	14	2	AAR76277	Aar76277 Bacterial
643	27	27.6	14	2	AAR76452	Aar76452 Bacterial
644	27	27.6	14	2	AAW06067	Aaw06067 Recombina
645	27	27.6	14	2	AAW06068	Aaw06068 Recombina
646	27	27.6	14	2	AAW05886	Aaw05886 Recombina
647	27	27.6	14	2	AAW04069	Aaw04069 Antifunga
648	27	27.6	14	2	AAW04143	Aaw04143 Antifunga
649	27	27.6	14	2	AAW04142	Aaw04142 Antifunga
650	27	27.6	14	2	AAW44406	Aaw44406 Anti-fung
651	27	27.6	14	2	AAW44508	Aaw44508 Anti-fung
652	27	27.6	14	2	AAW44507	Aaw44507 Anti-fung
653	27	27.6	14	2	AAW43694	Aaw43694 Bacterici
654	27	27.6	14	2	AAW43589	Aaw43589 Bacterici
655	27	27.6	14	2	AAW43693	Aaw43693 Bacterici
656	27	27.6	14	2	AAW58654	Aaw58654 Platelet
657	27	27.6	14	2	AAW63518	Aaw63518 Human BPI
658	27	27.6	14	2	AAW63519	Aaw63519 Human BPI
659	27	27.6	14	2	AAW63337	Aaw63337 Human BPI
660	27	27.6	14	2	AAY01187	Aay01187 Polypepti
661	27	27.6	14	2	AAY00485	Aay00485 Antifunga
662	27	27.6	14	2	AAY00383	Aay00383 Antifunga
663	27	27.6	14	2	AAY00484	Aay00484 Antifunga
664	27	27.6	14	3	AAB16258	Aab16258 Bacterici
665	27	27.6	14	3	AAB16259	Aab16259 Bacterici
666	27	27.6	14	3	AAB16074	Aab16074 Bacterici
667	27	27.6	14	4	AAM97026	Aam97026 Human pep
668	27	27.6	14	4	AAB65408	Aab65408 Anti-fung
669	27	27.6	14	4	AAB65409	Aab65409 Anti-fung
670	27	27.6	14	4	AAB65307	Aab65307 Anti-fung
671	27	27.6	14	4	AAB68706	Aab68706 Peptide-b
672	27	27.6	14	4	AAB52428	Aab52428 Peptide B
673	27	27.6	14	4	AAB52429	Aab52429 Peptide B
674	27	27.6	14	4	AAB52244	Aab52244 Peptide B
675	27	27.6	14	8	ADI66718	Adi66718 Rat bacte
676	27	27.6	14	8	ADI66719	Adi66719 Rat bacte
677	27	27.6	14	8	ADI66537	Adi66537 Rat bacte
678	27	27.6	14	8	ADM91451	Adm91451 Bacterici
679	27	27.6	14	8	ADM91450	Adm91450 Bacterici
680	27	27.6	14	8	ADM91349	Adm91349 Bacterici
681	27	27.6	15	1	AAP70354	Aap70354 Sequence
682	27	27.6	15	4	AAG64381	Aag64381 Human act
683	27	27.6	15	6	ABR32250	Abr32250 Human can

684	27	27.6	15	6	ABR31879	Abr31879 Human can
685	27	27.6	15	6	ABR32222	Abr32222 Human can
686	27	27.6	15	8	ADV32024	Adv32024 Human 109
687	27	27.6	15	8	ADV31996	Adv31996 Human 109
688	27	27.6	15	9	AEB12248	Aeb12248 Cyclin A
689	27	27.6	15	9	AEB12244	Aeb12244 Cyclin A
690	27	27.6	15	9	AEB12247	Aeb12247 Cyclin A
691	27	27.6	15	9	AEC70708	Aec70708 Human 109
692	27	27.6	15	9	AEC71051	Aec71051 Human 109
693	27	27.6	15	9	AEC71079	Aec71079 Human 109
694	27	27.6	16	2	AAR64603	Aar64603 RF-1 pept
695	27	27.6	16	2	AAW59266	Aaw59266 Myc-tag p
696	27	27.6	16	4	AAB55206	Aab55206 Anti-RSV
697	27	27.6	16	5	AAE18707	Aae18707 Major his
698	27	27.6	16	8	ADI41392	Adi41392 Human HGP
699	27	27.6	17	2	AAW14812	Aaw14812 sis oncog
700	27	27.6	17	2	AAW14830	Aaw14830 PDGF-2 on
701	27	27.6	17	2	AAR73655	Aar73655 PDGF(73-8
702	27	27.6	17	2	AAR73665	Aar73665 Cyclic PD
703	27	27.6	17	2	AAR64604	Aar64604 RF-1 pept
704	27	27.6	17	3	AAY52611	Aay52611 v-sis enc
705	27	27.6	17	4	AAB55207	Aab55207 Anti-RSV
706	27	27.6	17	5	AAU82600	Aau82600 Llama CDR
707	27	27.6	17	8	ADO42136	Ado42136 Marburg i
708	27	27.6	18	2	AAR22589	Aar22589 Nonlinear
709	27	27.6	18	2	AAR73656	Aar73656 PDGF(73-8
710	27	27.6	18	2	AAR73657	Aar73657 Ac-PDGF(7
711	27	27.6	18	2	AAR64605	Aar64605 RF-1 pept
712	27	27.6	18	2	AAR85995	Aar85995 Pro-endot
713	27	27.6	18	4	AAB55208	Aab55208 Anti-RSV
714	27	27.6	18	6	ABU03297	Abu03297 Human exp
715	27	27.6	18	9	AED68532	Aed68532 Antimicro
716	27	27.6	18	10	AEF01917	Aef01917 Ii-key/ H
717	27	27.6	18	10	AEF01959	Aef01959 Ii-key/ H
718	27	27.6	18	10	AEF01944	Aef01944 Ii-key/ H
719	27	27.6	19	2	AAR64606	Aar64606 RF-1 pept
720	27	27.6	19	3	AAY65729	Aay65729 Breast ca
721	27	27.6	19	4	AAB55209	Aab55209 Anti-RSV
722	27	27.6	19	6	ABP58053	Abp58053 Collagen
723	27	27.6	20	2	AAR64607	Aar64607 RF-1 pept
724	27	27.6	20	2	AAW12307	Aaw12307 Immunogen
725	27	27.6	20	2	AAW30098	Aaw30098 Neurotran
726	27	27.6	20	2	AAW62866	Aaw62866 Epitope o
727	27	27.6	20	4	AAB55210	Aab55210 Anti-RSV
728	27	27.6	20	4	AAE12829	Aae12829 Human MHC
729	27	27.6	20	6	ABP55284	Abp55284 Human mus
730	27	27.6	20	8	ADS17221	Ads17221 Peptide #
731	27	27.6	20	8	ADS17222	Ads17222 MHC Class
732	27	27.6	21	2	AAR64608	Aar64608 RF-1 pept
733	27	27.6	21	3	AAY89352	Aay89352 Core poly
734	27	27.6	21	3	AAY89225	Aay89225 Core poly
735	27	27.6	21	4	AAB55211	Aab55211 Anti-RSV
736	27	27.6	21	4	AAB77578	Aab77578 Core poly
737	27	27.6	21	4	AAB77753	Aab77753 Core poly
738	27	27.6	21	4	ABB02059	Abb02059 Viral cor
739	27	27.6	21	4	ABB02236	Abb02236 Viral cor
740	27	27.6	21	4	ABB00583	Abb00583 RSV F1 pr
741	27	27.6	21	4	ABB00760	Abb00760 Viral DP1
742	27	27.6	21	4	AAU13131	Aau13131 DP178-lik
743	27	27.6	21	4	AAU13306	Aau13306 DP178-lik
744	27	27.6	21	5	ADE02079	Ade02079 Hybrid po

745	27	27.6	21	5	ADE02256	Ade02256 Hybrid po
746	27	27.6	21	7	ADC17642	Adc17642 Type IV c
747	27	27.6	21	7	ADF30617	Adf30617 Rat angio
748	27	27.6	21	8	ADR19164	Adr19164 Type IV c
749	27	27.6	22	2	AAR48546	Aar48546 Sequence
750	27	27.6	22	2	AAR64609	Aar64609 RF-1 pept
751	27	27.6	22	2	AAW47933	Aaw47933 Antigenic
752	27	27.6	22	2	AAY18824	Aay18824 Lecithin:
753	27	27.6	22	2	AAY18853	Aay18853 Lecithin:
754	27	27.6	22	2	AAY18846	Aay18846 Lecithin:
755	27	27.6	22	2	AAY18856	Aay18856 Lecithin:
756	27	27.6	22	2	AAY18789	Aay18789 Lecithin:
757	27	27.6	22	2	AAY18867	Aay18867 Lecithin:
758	27	27.6	22	2	AAY18825	Aay18825 Lecithin:
759	27	27.6	22	2	AAY18836	Aay18836 Lecithin:
760	27	27.6	22	2	AAY18830	Aay18830 Lecithin:
761	27	27.6	22	2	AAY18828	Aay18828 Lecithin:
762	27	27.6	22	2	AAY18858	Aay18858 Lecithin:
763	27	27.6	22	2	AAY18865	Aay18865 Lecithin:
764	27	27.6	22	2	AAY18854	Aay18854 Lecithin:
765	27	27.6	22	2	AAY18860	Aay18860 Lecithin:
766	27	27.6	22	2	AAY18710	Aay18710 Lecithin:
767	27	27.6	22	2	AAY18759	Aay18759 Lecithin:
768	27	27.6	22	2	AAY18832	Aay18832 Lecithin:
769	27	27.6	22	2	AAY18834	Aay18834 Lecithin:
770	27	27.6	22	2	AAY18829	Aay18829 Lecithin:
771	27	27.6	22	2	AAY18835	Aay18835 Lecithin:
772	27	27.6	22	2	AAY18838	Aay18838 Lecithin:
773	27	27.6	22	2	AAY18823	Aay18823 Lecithin:
774	27	27.6	22	2	AAY18833	Aay18833 Lecithin:
775	27	27.6	22	2	AAY18847	Aay18847 Lecithin:
776	27	27.6	22	2	AAY18868	Aay18868 Lecithin:
777	27	27.6	22	2	AAY18831	Aay18831 Lecithin:
778	27	27.6	22	2	AAY18703	Aay18703 Lecithin:
779	27	27.6	22	2	AAY18772	Aay18772 Lecithin:
780	27	27.6	22	2	AAY19085	Aay19085 Lecithin:
781	27	27.6	22	2	AAY19108	Aay19108 Lecithin:
782	27	27.6	22	2	AAY19121	Aay19121 Lecithin:
783	27	27.6	22	2	AAY19087	Aay19087 Lecithin:
784	27	27.6	22	2	AAY19092	Aay19092 Lecithin:
785	27	27.6	22	2	AAY19101	Aay19101 Lecithin:
786	27	27.6	22	2	AAY19078	Aay19078 Lecithin:
787	27	27.6	22	2	AAY19112	Aay19112 Lecithin:
788	27	27.6	22	2	AAY19119	Aay19119 Lecithin:
789	27	27.6	22	2	AAY18964	Aay18964 Lecithin:
790	27	27.6	22	2	AAY19084	Aay19084 Lecithin:
791	27	27.6	22	2	AAY19107	Aay19107 Lecithin:
792	27	27.6	22	2	AAY19026	Aay19026 Lecithin:
793	27	27.6	22	2	AAY19090	Aay19090 Lecithin:
794	27	27.6	22	2	AAY18957	Aay18957 Lecithin:
795	27	27.6	22	2	AAY19079	Aay19079 Lecithin:
796	27	27.6	22	2	AAY19086	Aay19086 Lecithin:
797	27	27.6	22	2	AAY19110	Aay19110 Lecithin:
798	27	27.6	22	2	AAY19122	Aay19122 Lecithin:
799	27	27.6	22	2	AAY19043	Aay19043 Lecithin:
800	27	27.6	22	2	AAY19077	Aay19077 Lecithin:
801	27	27.6	22	2	AAY19083	Aay19083 Lecithin:
802	27	27.6	22	2	AAY19114	Aay19114 Lecithin:
803	27	27.6	22	2	AAY19089	Aay19089 Lecithin:
804	27	27.6	22	2	AAY19013	Aay19013 Lecithin:
805	27	27.6	22	2	AAY19082	Aay19082 Lecithin:

806	27	27.6	22	2	AAY19088	Aay19088 Lecithin:
807	27	27.6	22	2	AAY19100	Aay19100 Lecithin:
808	27	27.6	22	2	AAY19376	Aay19376 Lecithin:
809	27	27.6	22	2	AAY19211	Aay19211 Lecithin:
810	27	27.6	22	2	AAY19267	Aay19267 Lecithin:
811	27	27.6	22	2	AAY19355	Aay19355 Lecithin:
812	27	27.6	22	2	AAY19361	Aay19361 Lecithin:
813	27	27.6	22	2	AAY19373	Aay19373 Lecithin:
814	27	27.6	22	2	AAY19338	Aay19338 Lecithin:
815	27	27.6	22	2	AAY19332	Aay19332 Lecithin:
816	27	27.6	22	2	AAY19346	Aay19346 Lecithin:
817	27	27.6	22	2	AAY19364	Aay19364 Lecithin:
818	27	27.6	22	2	AAY19331	Aay19331 Lecithin:
819	27	27.6	22	2	AAY19339	Aay19339 Lecithin:
820	27	27.6	22	2	AAY19354	Aay19354 Lecithin:
821	27	27.6	22	2	AAY19218	Aay19218 Lecithin:
822	27	27.6	22	2	AAY19337	Aay19337 Lecithin:
823	27	27.6	22	2	AAY19342	Aay19342 Lecithin:
824	27	27.6	22	2	AAY19297	Aay19297 Lecithin:
825	27	27.6	22	2	AAY19362	Aay19362 Lecithin:
826	27	27.6	22	2	AAY19340	Aay19340 Lecithin:
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828	27	27.6	22	2	AAY19343	Aay19343 Lecithin:
829	27	27.6	22	2	AAY19344	Aay19344 Lecithin:
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831	27	27.6	22	2	AAY19333	Aay19333 Lecithin:
832	27	27.6	22	2	AAY19280	Aay19280 Lecithin:
833	27	27.6	22	2	AAY19336	Aay19336 Lecithin:
834	27	27.6	22	2	AAY19341	Aay19341 Lecithin:
835	27	27.6	22	2	AAY19368	Aay19368 Lecithin:
836	27	27.6	22	2	AAY18565	Aay18565 Lecithin:
837	27	27.6	22	2	AAY18569	Aay18569 Lecithin:
838	27	27.6	22	2	AAY18597	Aay18597 Lecithin:
839	27	27.6	22	2	AAY18496	Aay18496 Lecithin:
840	27	27.6	22	2	AAY18567	Aay18567 Lecithin:
841	27	27.6	22	2	AAY18583	Aay18583 Lecithin:
842	27	27.6	22	2	AAY18561	Aay18561 Lecithin:
843	27	27.6	22	2	AAY18571	Aay18571 Lecithin:
844	27	27.6	22	2	AAY18590	Aay18590 Lecithin:
845	27	27.6	22	2	AAY18568	Aay18568 Lecithin:
846	27	27.6	22	2	AAY18509	Aay18509 Lecithin:
847	27	27.6	22	2	AAY18572	Aay18572 Lecithin:
848	27	27.6	22	2	AAY18560	Aay18560 Lecithin:
849	27	27.6	22	2	AAY18526	Aay18526 Lecithin:
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852	27	27.6	22	2	AAY18591	Aay18591 Lecithin:
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858	27	27.6	22	2	AAY18566	Aay18566 Lecithin:
859	27	27.6	22	2	AAY18593	Aay18593 Lecithin:
860	27	27.6	22	2	AAY18595	Aay18595 Lecithin:
861	27	27.6	22	2	AAY18602	Aay18602 Lecithin:
862	27	27.6	22	2	AAY18447	Aay18447 Lecithin:
863	27	27.6	22	2	AAY18584	Aay18584 Lecithin:
864	27	27.6	22	4	AAB55212	Aab55212 Anti-RSV
865	27	27.6	22	7	ADD88522	Add88522 Influenza
866	27	27.6	22	7	ADG18287	Adg18287 Influenza

867	27	27.6	22	8	ADG21051	Adg21051 Apolipopr
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870	27	27.6	22	8	ADG21042	Adg21042 Apolipopr
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872	27	27.6	22	8	ADG21006	Adg21006 Apolipopr
873	27	27.6	22	8	ADG21040	Adg21040 Apolipopr
874	27	27.6	22	8	ADG21050	Adg21050 Apolipopr
875	27	27.6	22	8	ADG21045	Adg21045 Apolipopr
876	27	27.6	22	8	ADG21053	Adg21053 Apolipopr
877	27	27.6	22	8	ADG20927	Adg20927 Apolipopr
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886	27	27.6	22	8	ADG21049	Adg21049 Apolipopr
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902	27	27.6	22	8	ADJ32931	Adj32931 Apo lipop
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905	27	27.6	22	8	ADJ33013	Adj33013 Apo lipop
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908	27	27.6	22	8	ADJ32984	Adj32984 Apo lipop
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913	27	27.6	22	8	ADJ32988	Adj32988 Apo lipop
914	27	27.6	22	8	ADJ32994	Adj32994 Apo lipop
915	27	27.6	22	8	ADJ33019	Adj33019 Apo lipop
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917	27	27.6	22	8	ADJ32991	Adj32991 Apo lipop
918	27	27.6	22	8	ADJ33024	Adj33024 Apo lipop
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920	27	27.6	22	8	ADJ32997	Adj32997 Apo lipop
921	27	27.6	22	8	ADJ33005	Adj33005 Apo lipop
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923	27	27.6	22	9	ADW92449	Adw92449 H1N1 infl
924	27	27.6	23	2	AAR64610	Aar64610 RF-1 pept
925	27	27.6	23	2	AAY07215	Aay07215 Peptide t
926	27	27.6	23	3	AAY89232	Aay89232 Core poly
927	27	27.6	23	3	AAY89499	Aay89499 Core poly

928	27	27.6	23	4	AAB55213	Aab55213 Anti-RSV
929	27	27.6	23	4	AAB77585	Aab77585 Core poly
930	27	27.6	23	4	AAB77900	Aab77900 Core poly
931	27	27.6	23	4	AAB77901	Aab77901 Core poly
932	27	27.6	23	4	ABB00908	Abb00908 Viral DP1
933	27	27.6	23	4	ABB02374	Abb02374 Viral cor
934	27	27.6	23	4	ABB02375	Abb02375 Viral cor
935	27	27.6	23	4	ABB00907	Abb00907 Viral DP1
936	27	27.6	23	4	ABB00590	Abb00590 RSV F1 pr
937	27	27.6	23	4	ABB02066	Abb02066 Viral cor
938	27	27.6	23	4	AAU13138	Aau13138 DP178-lik
939	27	27.6	23	4	AAU13453	Aau13453 DP178-lik
940	27	27.6	23	5	ADE02394	Ade02394 Hybrid po
941	27	27.6	23	5	ADE02086	Ade02086 Hybrid po
942	27	27.6	23	5	ADE02395	Ade02395 Hybrid po
943	27	27.6	23	10	AEF20484	Aef20484 Human ost
944	27	27.6	24	2	AAR64611	Aar64611 RF-1 pept
945	27	27.6	24	2	AAW33941	Aaw33941 Beta1-adr
946	27	27.6	24	3	AAY89500	Aay89500 Core poly
947	27	27.6	24	4	AAB55214	Aab55214 Anti-RSV
948	27	27.6	24	4	AAM86218	Aam86218 Human imm
949	27	27.6	24	4	AAB70120	Aab70120 Penicilli
950	27	27.6	24	4	AAU13454	Aau13454 DP178-lik
951	27	27.6	25	2	AAR64612	Aar64612 RF-1 pept
952	27	27.6	25	2	AAW30494	Aaw30494 Flea sali
953	27	27.6	25	3	AAY89231	Aay89231 Core poly
954	27	27.6	25	3	AAY89237	Aay89237 Core poly
955	27	27.6	25	4	AAB55215	Aab55215 Anti-RSV
956	27	27.6	25	4	ABB40984	Abb40984 Peptide #
957	27	27.6	25	4	ABB43082	Abb43082 Peptide #
958	27	27.6	25	4	AAM34759	Aam34759 Peptide #
959	27	27.6	25	4	AAM36907	Aam36907 Peptide #
960	27	27.6	25	4	AAB77590	Aab77590 Core poly
961	27	27.6	25	4	AAB77584	Aab77584 Core poly
962	27	27.6	25	4	AAM76801	Aam76801 Human bon
963	27	27.6	25	4	AAM63981	Aam63981 Human bra
964	27	27.6	25	4	AAM61844	Aam61844 Human bra
965	27	27.6	25	4	ABG58482	Abg58482 Human liv
966	27	27.6	25	4	ABB00595	Abb00595 RSV F1 pr
967	27	27.6	25	4	ABB02071	Abb02071 Viral cor
968	27	27.6	25	4	ABB02065	Abb02065 Viral cor
969	27	27.6	25	4	ABB00589	Abb00589 RSV F1 pr
970	27	27.6	25	4	AAU13143	Aau13143 DP178-lik
971	27	27.6	25	4	AAU13137	Aau13137 DP178-lik
972	27	27.6	25	5	ADE02085	Ade02085 Hybrid po
973	27	27.6	25	5	ADE02091	Ade02091 Hybrid po
974	27	27.6	25	7	ADC26852	Adc26852 B. burgdo
975	27	27.6	25	9	ADV57496	Adv57496 G protein
976	27	27.6	25	9	ADV55203	Adv55203 G protein
977	27	27.6	25	9	ADV56698	Adv56698 G protein
978	27	27.6	25	9	ADV55545	Adv55545 G protein
979	27	27.6	25	9	ADZ38618	Adz38618 Group A S
980	27	27.6	26	2	AAR64613	Aar64613 RF-1 pept
981	27	27.6	26	4	AAB55216	Aab55216 Anti-RSV
982	27	27.6	26	10	AEE38856	Aee38856 Human ser
983	27	27.6	27	2	AAR50607	Aar50607 G-protein
984	27	27.6	27	2	AAR64614	Aar64614 RF-1 pept
985	27	27.6	27	2	AAW02799	Aaw02799 G-protein
986	27	27.6	27	2	AAW82353	Aaw82353 Flea sali
987	27	27.6	27	3	AAY89236	Aay89236 Core poly
988	27	27.6	27	3	AAY89230	Aay89230 Core poly

RESULT 4
ADZ69803
ID ADZ69803 standard; peptide; 9 AA.
XX
AC ADZ69803;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:78.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 78; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 9 AA;

  Query Match   43.9%; Score 43; DB 9; Length 9;
  Best Local Similarity   100.0%; Pred. No. 2.1e+06;
  Matches   9; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          7 VNTQIDLIR 15
              |||||||||
Db          1 VNTQIDLIR 9
```

715-733

RESULT 3
ADY20753
ID ADY20753 standard; peptide; 12 AA.
XX
AC ADY20753;
XX
DT 05-MAY-2005 (first entry)
XX
DE Botulinum peptide fragment #1.
XX
KW Delivery mechanism; toxin; endocytosis; bacterial infection;
KW viral infection; antibacterial; virucide.
XX
OS Unidentified.
XX
PN WO2005014798-A2.
XX
PD 17-FEB-2005.
XX
PF 31-MAR-2004; 2004WO-US009829.
XX
PR 31-MAR-2003; 2003US-0459185P.
XX
PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Murphy JR, Ratts R, Pearson DA;
XX
DR WPI; 2005-173098/18.
XX
PT New compound, useful in the manufacture of a medicament for inhibiting
PT cell death or the translocation of a viral or bacterial toxin or viral
PT transcription factor for treating or preventing bacterial or viral
PT infections.
XX
PS Disclosure; Fig 9; 100pp; English.
XX
CC The invention relates to a new peptide compound and a nucleic acid
CC sequence encoding the peptide. The invention also relates to a method of
CC identifying a compound that inhibits cell death in a mammal and a method
CC of identifying a compound that promotes cell death in a mammal. The
CC compound is useful in the manufacture of a medicament for inhibiting cell
CC death in a mammal. The compound inhibits the translocation of a viral or
CC bacterial toxin from the lumen of an endosome to the cytosol of the cell
CC or the translocation of a viral or retroviral transcription factor. The
CC compound is further reacted with a monoclonal antibody, or its fragment
CC to form a covalent bond between a sulfur atom of the antibody and the
CC maleimide group of the compound. Identifying a compound that inhibits
CC cell death in a mammal comprises isolating endosomes from the cell,
CC placing the endosomes in a cytosolic buffer, contacting the endosomes
CC with a fusion protein-toxin, where the protein comprises a binding moiety
CC for a component of the cell membrane of the cell and the toxin comprises
CC a fragment of Diphtheria toxin, contacting the endosomes with a cytosolic
CC translocation factor complex, contacting the endosomes with the compound
CC and measuring translocation of the toxin, where a decreased level of the
CC translocation relative to that observed in the absence of the compound
CC indicates that the compound inhibits the cell death. Identifying a
CC compound that promotes cell death in a mammal comprises isolating
CC endosomes from the cell, placing the endosomes in a cytosolic buffer,
CC contacting the endosomes with a fusion protein-toxin, where the protein
CC comprises a binding moiety for a component of the cell membrane of the
CC cell and the toxin comprises a fragment of Diphtheria toxin, contacting

CC the endosomes with a cytosolic translocation factor complex, contacting
CC the endosomes with the compound and measuring translocation of the toxin,
CC where an increased level of the translocation relative to that observed
CC in the absence of the compound indicates that the compound promotes the
CC cell death. The compound is useful in the manufacture of a medicament for
CC inhibiting cell death in a mammal or for inhibiting the translocation of
CC a viral or bacterial toxin, e.g., Diphtheria toxin, a Botulinum toxin,
CC Anthrax toxin LF or Anthrax toxin EF from the lumen of an endosome to the
CC cytosol of the cell or the translocation of a viral or retroviral
CC transcription factor, e.g., human immunodeficiency virus reverse
CC transcriptase or Tat for treating or preventing bacterial or viral
CC infections. This sequence represents a botulinum peptide fragment used in
CC the scope of the invention.
XX
SQ Sequence 12 AA;

Query Match 53.1%; Score 52; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          5 AKVNTQIDLIR 15
              ||||||||||
Db          1 AKVNTQIDLIR 11
```

RESULT 47
ABP68020
ID ABP68020 standard; peptide; 12 AA.
XX
AC ABP68020;
XX
DT 08-JAN-2003 (first entry)
XX
DE Bacillus thuringiensis toxin Cry related peptide #13.
XX
KW Bacillus thuringiensis; insecticide; toxin; Cry; pepsin cleavage site;
KW pepsin; PCS.
XX
OS Bacillus thuringiensis.
OS Synthetic.
XX
PN FR2822157-A1.
XX
PD 20-SEP-2002.
XX
PF 19-MAR-2001; 2001FR-00003691.
XX
PR 19-MAR-2001; 2001FR-00003691.
XX
PA (AVET) AVENTIS CROPSCIENCE SA.
XX
PI Freyssinet G, Rang C, Frutos R;
XX
DR WPI; 2003-002439/01.
XX
PT New modified Cry protein, useful as insecticide, comprises at least one
PT additional pepsin cleavage site to reduce persistence in mammalian gut.
XX
PS Example 2; Page 21; 134pp; French.
XX
CC The present invention describes a modified Cry protein (I) that is
CC sensitive to pepsin and comprises at least one additional pepsin cleavage
CC site (PCS). Also described: (a) increasing pepsin sensitivity of Cry
CC proteins by incorporating at least one extra PCS; (b) polynucleotides
CC (II) that encode (I); (c) chimeric genes (CG) that contain a promoter,
CC (II) and terminator; (d) expression or transformation vector (III) that
CC contains CG; (e) host organism (IV) transformed with (III), also, where
CC the organism is a plant, its parts and seeds; (f) production of (I) by
CC growing (IV); and (g) mono- or polyclonal antibodies (Ab) directed
CC against (I). (I) has insecticide activity. (I) can be used as
CC insecticides, particularly where expressed in transgenic plants. (I) are
CC sensitive to enzymes in the digestive tract of mammals, so do not persist
CC in the tract (lack of persistence is required by regulatory authorities
CC for use, in foods, of seeds containing Cry proteins). Extra PCS do not
CC increase degradation in the digestive tract of insects, so have no effect
CC on insecticidal activity. ABV93450 to ABV93909 and ABP67997 to ABP68308
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 12 AA;

715-733

Query Match 33.7%; Score 33; DB 6; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 NWLAKVN 8
              ||||::|
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Db 2 NWLAELN 8

dem93
673-691

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RESULT 48
US-10-506-877-32
; Sequence 32, Application US/10506877
; Publication No. US20060148093A1
; GENERAL INFORMATION:
;  APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
;  TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF MODIFIED PROTEINS
;  FILE REFERENCE: 56954 PCT (70207)
;  CURRENT APPLICATION NUMBER: US/10/506,877
;  CURRENT FILING DATE:  2004-09-03
;  PRIOR APPLICATION NUMBER: 60/363,179
;  PRIOR FILING DATE: 2002-03-11
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphopeptide sequence
US-10-506-877-32

  Query Match             27.5%;  Score 25;  DB 6;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 9.2e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 VSYIAN 15
              :||:||
Db          7 LSYVAN 12
```

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OM protein - protein search, using sw model

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Title: US-10-821-669-1_COPY_715_733
Perfect score: 98
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Maximum Match 100%
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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	98	100.0	19	9	ADW11060	Adw11060 Clostridi
2	98	100.0	27	9	ADW11113	Adw11113 Clostridi
3	52	53.1	12	9	ADY20753	Ady20753 Botulinum
4	43	43.9	9	9	ADZ69803	Adz69803 Botulinum
5	38.5	39.3	22	2	AAY18841	Aay18841 Lecithin:
6	38.5	39.3	22	2	AAY19095	Aay19095 Lecithin:
7	38.5	39.3	22	2	AAY19349	Aay19349 Lecithin:
8	38.5	39.3	22	2	AAY18578	Aay18578 Lecithin:
9	38.5	39.3	22	8	ADG21058	Adg21058 Apolipopr
10	38.5	39.3	22	8	ADJ33000	Adj33000 Apo lipop
11	38	38.8	22	2	AAY18741	Aay18741 Lecithin:
12	38	38.8	22	2	AAY18995	Aay18995 Lecithin:
13	38	38.8	22	2	AAY19249	Aay19249 Lecithin:
14	38	38.8	22	2	AAY18478	Aay18478 Lecithin:
15	38	38.8	22	8	ADG20958	Adg20958 Apolipopr
16	38	38.8	22	8	ADJ32900	Adj32900 Apo lipop
17	36	36.7	22	2	AAR48545	Aar48545 Sequence
18	36	36.7	22	9	AEB28559	Aeb28559 Human apo
19	36	36.7	22	9	AEB11518	Aeb11518 Apolipopr
20	35	35.7	9	9	ADZ69802	Adz69802 Botulinum

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 13:29:52 ; Search time 19 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-10-821-669-1_COPY_715_733
Perfect score: 98
Sequence: 1 TNWLAKVNTQIDLIRKKMK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 331034

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

715-733

```
RESULT 1
US-10-715-810-78
; Sequence 78, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 721-729)
US-10-715-810-78

  Query Match           43.9%;  Score 43;  DB 5;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 VNTQIDLIR 15
              |||||||||
Db          1 VNTQIDLIR 9
```

715-733

```
RESULT 25
US-10-946-371-30
; Sequence 30, Application US/10946371
; Publication No. US20050208587A1
; GENERAL INFORMATION:
;  APPLICANT: CARDOSO, ROSA
;  APPLICANT:  WILSON, IAN
;  APPLICANT:  BURTON, DENNIS
;  APPLICANT:  DAWSON, PHILIP
;  TITLE OF INVENTION: PEPTIDES THAT BIND TO BROADLY NEUTRALIZING ANTI-HIV
;  TITLE OF INVENTION:  ANTIBODY-STRUCTURE OF 4E10 FAB FRAGMENT COMPLEX, USES
;  TITLE OF INVENTION:  THEREOF, COMPOSITIONS THEREFROM
;  FILE REFERENCE: 678501-2001.1
;  CURRENT APPLICATION NUMBER: US/10/946,371
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: 60/504,123
;  PRIOR FILING DATE: 2003-09-19
;  PRIOR APPLICATION NUMBER: PCT/EP02/10070
;  PRIOR FILING DATE: 2002-09-09
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 30
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-10-946-371-30

  Query Match             35.7%;  Score 35;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||||
Db          6 TNWLAK 11
```

```
RESULT 24
US-10-715-810-77
; Sequence 77, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 712-720)
US-10-715-810-77

  Query Match          35.7%;  Score 35;  DB 5;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||||
Db          4 TNWLAK 9
```

```
RESULT 22
ADY81603
ID   ADY81603 standard; peptide; 15 AA.
XX
AC   ADY81603;
XX
DT   16-JUN-2005  (first entry)
XX
DE   HIV-1 antibody 4E10 binding peptide #21.
XX
KW   diagnosis; pharmaceutical; immunogenicity; immunostimulant; anti-HIV;
KW   vaccine.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO2005028499-A2.
XX
PD   31-MAR-2005.
XX
PF   20-SEP-2004; 2004WO-US030747.
XX
PR   19-SEP-2003; 2003US-0504123P.
XX
PA   (SCRI ) SCRIPPS RES INST.
XX
PI   Cardoso R,  Wilson I,  Burton D,  Dawson P;
XX
DR   WPI; 2005-254114/26.
XX
PT   New Fab 4E10:KGND complex having an X-ray diffraction pattern, useful for
PT   eliciting antibodies or in a diagnostic, pharmaceutical immunogenic,
PT   immunological or vaccine composition.
XX
PS   Claim 46; Page 115; 190pp; English.
XX
CC   The invention relates to a Fab 4E10:KGND complex having an X-ray
CC   diffraction pattern corresponding to or resulting from any or all of
CC   those given in the specification and having the structure defined by the
CC   coordinates listed in the specification. The complex is useful for
CC   eliciting antibodies or in a diagnostic, pharmaceutical immunogenic,
CC   immunological or vaccine composition. The present sequence represents the
CC   HIV-1 antibody 4E10 binding peptide.
XX
SQ   Sequence 15 AA;

  Query Match             35.7%;  Score 35;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||||
Db          7 TNWLAK 12
```

```
RESULT 20
US-11-416-262-10
; Sequence 10, Application US/11416262
; Publication No. US20060191547A1
; GENERAL INFORMATION:
;  APPLICANT: Conkling, Mark
;  TITLE OF INVENTION: MODIFYING NICOTINE AND NITROSAMINE
;  TITLE OF INVENTION:  LEVELS IN TOBACCO
;  FILE REFERENCE: VTOB.033C2C
;  CURRENT APPLICATION NUMBER: US/11/416,262
;  CURRENT FILING DATE:  2006-05-01
;  PRIOR APPLICATION NUMBER: 11/077,752
;  PRIOR FILING DATE: 2005-03-10
;  PRIOR APPLICATION NUMBER: 10/729,121
;  PRIOR FILING DATE: 2003-12-05
;  PRIOR APPLICATION NUMBER: 60/297,154
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: PCTUS02/18040
;  PRIOR FILING DATE: 2002-06-06
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
US-11-416-262-10

  Query Match             28.6%;  Score 28;  DB 7;  Length 26;
  Best Local Similarity   66.7%;  Pred. No. 4.7e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||::
Db         18 TNWLSE 23
```

```
RESULT 23
US-11-439-071-36
; Sequence 36, Application US/11439071
; Publication No. US20060204492A1
;  GENERAL INFORMATION:
;    APPLICANT:  Huse, William D.
;    APPLICANT:  Glaser, Scott M.
;    TITLE OF INVENTION:  Anti-Alpha V Beta 3 Recombinant Human
;    TITLE OF INVENTION:  Antibodies, Nucleic Acids Encoding Same and Methods of Use
;    NUMBER OF SEQUENCES:  100
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/439,071
;      FILING DATE:  22-MAY-2006
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/016,061
;      FILING DATE:  30-JAN-1998
;      APPLICATION NUMBER:  US 08/791,391
;      FILING DATE:  30-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-IX 2965
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-11-439-071-36

  Query Match             27.6%;  Score 27;  DB 7;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 2.3e+02;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WLAKVNT 9
              |:|||::
Db          1 WVAKVSS 7
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```
RESULT 29
US-11-434-137-8322
; Sequence 8322, Application US/11434137
; Publication No. US20060210579A1
; GENERAL INFORMATION:
;  APPLICANT: Telford, John
;  APPLICANT:  Masignani, Vega
;  APPLICANT:  Ros, Immaculada Margarit Y
;  APPLICANT:  Fraser, Claire
;  APPLICANT:  Tettelin, Herve
;  TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/11/434,137
;  CURRENT FILING DATE:  2006-05-16
;  PRIOR APPLICATION NUMBER: US 10/415,182
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: PCT/GB01/04789
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: GB-0026333.5
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: GB-0028727.6
;  PRIOR FILING DATE: 2000-11-24
;  PRIOR APPLICATION NUMBER: GB-0105640.7
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 12025
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 8322
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Streptococcus pyogenes
US-11-434-137-8322

  Query Match             27.6%;  Score 27;  DB 7;  Length 30;
  Best Local Similarity   66.7%;  Pred. No. 8e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              |:||:|
Db          7 TSWLSK 12
```

```
RESULT 21
S42364
aromatic-amino-acid transaminase (EC 2.6.1.57) II [validated] - Thermococcus litoralis
C;Species: Thermococcus litoralis
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: S42364
R;Andreotti, G.; Cubellis, M.V.; Nitti, G.; Sannia, G.; Mai, X.; Marino, G.; Adams, M.
Eur. J. Biochem. 220, 543-549, 1994
A;Title: Characterization of aromatic aminotransferases from the hyperthermophilic arc
A;Reference number: S42354; MUID:94170805; PMID:8125113
A;Accession: S42364
A;Molecule type: protein
A;Residues: 1-30
A;Cross-references: UNIPROT:Q9UWK8; UNIPARC:UPI00000629CB
C;Superfamily: aspartate transaminase
C;Keywords: aminotransferase

  Query Match             24.5%;  Score 24;  DB 2;  Length 30;
  Best Local Similarity   50.0%;  Pred. No. 2.6e+03;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 NWLAKV 7
              :|:||:
Db         12 SWIAKL 17
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_743_761
Perfect score: 102
Sequence: 1 TKAIINYQYNQYTEEEKNN 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
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5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	19	9	ADW11062	Adw11062 Clostridi
2	102	100.0	27	9	ADW11114	Adw11114 Clostridi
3	80	78.4	15	9	ADZ69805	Adz69805 Botulinum

RESULT 30
AEF23970
ID AEF23970 standard; peptide; 10 AA.
XX
AC AEF23970;
XX
DT 09-MAR-2006 (first entry)
XX
DE Factor 8 inhibitor blocking peptide S2/74.
XX
KW Factor 8 inhibitor; vaccine; hemophilia A; Hemostatic.
XX
OS Synthetic.
XX
PN WO2006003183-A1.
XX
PD 12-JAN-2006.
XX
PF 01-JUL-2005; 2005WO-EP053139.
XX
PR 02-JUL-2004; 2004EP-00015586.
XX
PA (JUNG/) JUNGBAUER A.
XX
PI Jungbauer A;
XX
DR WPI; 2006-109510/11.
XX
PT New peptides that block the effects of factor 8 inhibitors, useful in the
PT treatment of hemophilia A.
XX
PS Claim 7; Page 24; 51pp; German.
XX
CC This invention describes novel peptides that block the effects of Factor
CC 8 inhibitors. The peptides contain at least two Tyr; at least one aa
CC that, under physiological conditions, carries a positive or negative
CC overall charge; at least one aa with a hydrophobic aromatic residue; at
CC the N-terminus one of Pro, Arg, Tyr or Phe; at the C-terminus one of Asp,
CC Arg, Lys, His or Phe; but no Cys and/or Val-Val. The peptides may be
CC conjugated to a compound that extends its half-life in vivo, e.g.
CC poly(ethylene glycol), dextran or agarose, and may include aa with the D-
CC configuration. The peptides block the autoantibodies/alloantibodies
CC directed against Factor 8, where these Ab inactivate Factor 8 so that
CC exogenously administered Factor 8 is no longer effective. When used as
CC vaccines they generate anti-idiotype antibodies that ensure long-term
CC protection. Since the peptides are relatively small, they block only the
CC binding site of Factor 8 inhibitors; they can interfere with inhibitory
CC antibodies having different epitope recognition patterns; generate an
CC immune response only against the epitope of interest; are easily prepared
CC ; are unlikely to induce an immune response or have significant side
CC effects, and only affected subjects need to be treated. The novel
CC peptides are useful for the treatment of hemophilia A.
XX
SQ Sequence 10 AA;

  Query Match   33.3%; Score 34; DB 10; Length 10;
  Best Local Similarity   71.4%; Pred. No. 2e+02;
  Matches   5; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

Qy   6 NYQYNQY 12
              :|||||:

```
Db          2 HYQYNQF 8
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```
RESULT 50
AEF23919
ID   AEF23919 standard; peptide; 10 AA.
XX
AC   AEF23919;
XX
DT   09-MAR-2006  (first entry)
XX
DE   Factor 8 inhibitor blocking peptide S2/23.
XX
KW   Factor 8 inhibitor; vaccine; hemophilia A; Hemostatic.
XX
OS   Synthetic.
XX
PN   WO2006003183-A1.
XX
PD   12-JAN-2006.
XX
PF   01-JUL-2005; 2005WO-EP053139.
XX
PR   02-JUL-2004; 2004EP-00015586.
XX
PA   (JUNG/) JUNGBAUER A.
XX
PI   Jungbauer A;
XX
DR   WPI; 2006-109510/11.
XX
PT   New peptides that block the effects of factor 8 inhibitors, useful in the
PT   treatment of hemophilia A.
XX
PS   Claim 7; Page 24; 51pp; German.
XX
CC   This invention describes novel peptides that block the effects of Factor
CC   8 inhibitors. The peptides contain at least two Tyr; at least one aa
CC   that, under physiological conditions, carries a positive or negative
CC   overall charge; at least one aa with a hydrophobic aromatic residue; at
CC   the N-terminus one of Pro, Arg, Tyr or Phe; at the C-terminus one of Asp,
CC   Arg, Lys, His or Phe; but no Cys and/or Val-Val. The peptides may be
CC   conjugated to a compound that extends its half-life in vivo, e.g.
CC   poly(ethylene glycol), dextran or agarose, and may include aa with the D-
CC   configuration. The peptides block the autoantibodies/alloantibodies
CC   directed against Factor 8, where these Ab inactivate Factor 8 so that
CC   exogenously administered Factor 8 is no longer effective. When used as
CC   vaccines they generate anti-idiotype antibodies that ensure long-term
CC   protection. Since the peptides are relatively small, they block only the
CC   binding site of Factor 8 inhibitors; they can interfere with inhibitory
CC   antibodies having different epitope recognition patterns; generate an
CC   immune response only against the epitope of interest; are easily prepared
CC   ; are unlikely to induce an immune response or have significant side
CC   effects, and only affected subjects need to be treated. The novel
CC   peptides are useful for the treatment of hemophilia A.
XX
SQ   Sequence 10 AA;

  Query Match             32.4%;  Score 33;  DB 10;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YQYNQY 12
              |||||:
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Db 3 YQYNQF 8

Search completed: November 1, 2006, 13:11:52
Job time : 112.564 secs

SCORE 1.3 BuildDate: 12/06/2005

```
RESULT 43
US-09-879-792-25
; Sequence 25, Application US/09879792
; Patent No. 6734006
; GENERAL INFORMATION:
;  APPLICANT: Xiao, Yonghong
;  APPLICANT:  Gedrich, Richard
;  TITLE OF INVENTION: Regulation of Human Transmembrane Serine
;  TITLE OF INVENTION:  Protease
;  FILE REFERENCE: 02973.00035
;  CURRENT APPLICATION NUMBER: US/09/879,792
;  CURRENT FILING DATE:  2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/211,224
;  PRIOR FILING DATE: 2000-06-13
;  PRIOR APPLICATION NUMBER: US 60/283,353
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: US 60/283,648
;  PRIOR FILING DATE: 2001-04-16
;  PRIOR APPLICATION NUMBER: PCT _________ (Docket No. 6734006 LIO-81-WO)
;  PRIOR FILING DATE: 2001-06-12
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: BLOCKS BL00495L
US-09-879-792-25

  Query Match             30.4%;  Score 31;  DB 2;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IINYQYN 10
              ||||:|:
Db          6 IINYEYD 12
```

```
RESULT 44
US-08-485-588-11
; Sequence 11, Application US/08485588
; Patent No. 5688938
;  GENERAL INFORMATION:
;    APPLICANT:  Edward M. Brown
;    APPLICANT:  Steven C. Hebert
;    APPLICANT:  Forrest H. Fuller
;    APPLICANT:  James E. Garrett, Jr.
;    TITLE OF INVENTION:  CALCIUM RECEPTOR-ACTIVE
;    TITLE OF INVENTION:  MOLECULES
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  First Interstate World Center
;      STREET:  Suite 4700
;      STREET:  633 West Fifth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  FASTSEQ
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,588
;      FILING DATE:  7 June, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:  9
;      APPLICATION NUMBER:  08/353,784
;      FILING DATE:  9 December, 1994
;      APPLICATION NUMBER:  PCT/US/94/12117
;      FILING DATE:  21 October, 1994
;      APPLICATION NUMBER:  U.S. 08/292,827
;      FILING DATE:  23 August, 1994
;      APPLICATION NUMBER:  U.S. 08/141,248
;      FILING DATE:  22 October, 1993
;      APPLICATION NUMBER:  U.S. 08/009,389
;      FILING DATE:  23 February, 1993
;      APPLICATION NUMBER:  U.S. 08/017,127
;      FILING DATE:  12 February, 1993
;      APPLICATION NUMBER:  U.S. 07/934,161
;      FILING DATE:  21 August, 1992
;      APPLICATION NUMBER:  U.S. 07/834,044
;      FILING DATE:  11 February, 1992
;      APPLICATION NUMBER:  U.S. 07/749,451
;      FILING DATE:  23 August, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Heber, Sheldon O.
;      REGISTRATION NUMBER:  38,179
;      REFERENCE/DOCKET NUMBER:  213/005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  19 amino acids
;      TYPE:  amino acids
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-485-588-11

  Query Match             30.4%;  Score 31;  DB 1;  Length 19;
  Best Local Similarity   62.5%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 NQYTEEEK 17
              :||::|||
Db          9 SQYSDEEK 16
```

```
RESULT 1
US-10-715-810-80
; Sequence 80, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 745-759)
US-10-715-810-80

  Query Match             78.4%;  Score 80;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AIINYQYNQYTEEEK 17
              |||||||||||||||
Db          1 AIINYQYNQYTEEEK 15
```

```
RESULT 31
US-10-526-062-15
; Sequence 15, Application US/10526062
; Publication No. US20060141563A1
; GENERAL INFORMATION:
;  APPLICANT: Biemans, Ralph
;  APPLICANT:  Denoel, Philippe
;  APPLICANT:  Feron, Christiane
;  APPLICANT:  Goraj, Karine
;  APPLICANT:  Kortekaas, Jeroen
;  APPLICANT:  Poolman, Jan
;  APPLICANT:  Tommassen, Jan
;  APPLICANT:  Weynants, Vincent
;  TITLE OF INVENTION: Mutant Protein and Refolding Method
;  FILE REFERENCE: VB60394
;  CURRENT APPLICATION NUMBER: US/10/526,062
;  CURRENT FILING DATE:  2005-02-28
;  PRIOR APPLICATION NUMBER: PCT/EP03/009634
;  PRIOR FILING DATE: 2003-08-28
;  PRIOR APPLICATION NUMBER: GB 0220199.4
;  PRIOR FILING DATE: 2002-08-30
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Neisseria meningitidis
US-10-526-062-15

  Query Match             27.5%;  Score 28;  DB 6;  Length 16;
  Best Local Similarity   83.3%;  Pred. No. 4e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TEEEKN 18
              |:||||
Db          1 TDEEKN 6
```

```
RESULT 25
JC2059
homeobox 4 protein - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C;Accession: JC2059
R;Feng, X.H.; Kung, S.D.
Biochem. Biophys. Res. Commun. 198, 1012-1019, 1994
A;Title: Identification of differentially expressed members of tobacco homeobox famili
A;Reference number: JC2057; MUID:94161708; PMID:7509595
A;Accession: JC2059
A;Molecule type: DNA
A;Residues: 1-19
A;Cross-references: UNIPROT:Q9SXV1; UNIPARC:UPI000017B0A8
A;Experimental source: leaf
C;Genetics:
A;Gene: Hot4
C;Keywords: homeobox

  Query Match             25.5%;  Score 26;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 EEEKN 18
              |||||
Db          1 EEEKN 5
```

```
RESULT 1
US-10-142-238A-70
; Sequence 70, Application US/10142238A
; Publication No. US20030087819A1
; GENERAL INFORMATION:
;  APPLICANT: Bielicki, John K.
;  TITLE OF INVENTION: CYSTEINE-CONTAINING PEPTIDES HAVING OXIDANT PROPERTIES
;  FILE REFERENCE: IB-1705
;  CURRENT APPLICATION NUMBER: US/10/142,238A
;  CURRENT FILING DATE:  2002-08-19
;  PRIOR APPLICATION NUMBER: US 60/289,944
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(22)
;   OTHER INFORMATION: HUMAN GENETIC ORIGIN
US-10-142-238A-70

  Query Match             43.0%;  Score 40;  DB 4;  Length 22;
  Best Local Similarity   43.8%;  Pred. No. 31;
  Matches    7;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 LNESINKAMININKFL 18
              | :|: : : |:||||
Db          3 LKDSLEQCLNNMNKFL 18
```

```
 Sequence 387, Application US/11199853
; Publication No. US20060216309A1
;  GENERAL INFORMATION:
;    APPLICANT:  David William Holden
;    TITLE OF INVENTION:  Identification of Genes
;    NUMBER OF SEQUENCES:  501
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/199,853
;      FILING DATE:  09-AUG-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/871,355
;      FILING DATE:  09-JUN-1997
;      APPLICATION NUMBER:  PCT/GB95/02875
;      FILING DATE:  11-DEC-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  RPMS 101 CON
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404) 873-8794
;      TELEFAX:  (404) 873-8795
;  INFORMATION FOR SEQ ID NO:  387:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  21 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
US-11-199-853-387

  Query Match             32.3%;  Score 30;  DB 7;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 ININKF 17
              ||:|||
Db         10 INVNKF 15
```

```
RESULT 37
S12171
H+-transporting two-sector ATPase (EC 3.6.3.14) lipid-binding protein - fission yeast
C;Species: mitochondrion Schizosaccharomyces pombe
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S12171
R;Massardo, D.R.
Nucleic Acids Res. 18, 6429, 1990
A;Title: Nucleotide sequence of the genes encoding tRNA(his), tRNA(pro) and tRNA(gln)
A;Reference number: S12171; MUID:91057135; PMID:2243789
A;Accession: S12171
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-14
A;Cross-references: UNIPROT:P21535; UNIPARC:UPI000016D64B; EMBL:X54552; NID:g13659; PI
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC2
C;Keywords: hydrolase; mitochondrion

  Query Match             23.7%;  Score 22;  DB 2;  Length 14;
  Best Local Similarity   50.0%;  Pred. No. 3.5e+03;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 LNESIN 8
              :|:|:|
Db          7 INDSLN 12
```

```
RESULT 32
P91713_DUGTI
ID   P91713_DUGTI   PRELIMINARY;   PRT;    27 AA.
AC   P91713;
DT   01-MAY-1997, integrated into UniProtKB/TrEMBL.
DT   01-MAY-1997, sequence version 1.
DT   07-FEB-2006, entry version 23.
DE   Homeodomain protein (Fragment).
GN   Name=DthoxB;
OS   Dugesia tigrina (Planarian).
OC   Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC   Paludicola; Dugesiidae; Girardia.
OX   NCBI_TaxID=6162;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97158715; PubMed=9006075;
RA   Bayascas J.R., Castillo E., Munoz-Marmol A.M., Salo E.B.;
RT   "Planarian Hox genes: novel patterns of expression during
RT   regeneration.";
RL   Development 124:141-148(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99016215; PubMed=9799427; DOI=10.1007/s004270050204;
RA   Bayascas J.R., Castillo E., Salo E.B.;
RT   "Platyhelminthes have a hox code differentially activated during
RT   regeneration, with genes closely related to those of spiralian
RT   protostomes.";
RL   Dev. Genes Evol. 208:467-473(1998).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X95415; CAA64695.1; -; Genomic_DNA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001356; Homeobox.
DR   Pfam; PF00046; Homeobox; 1.
DR   PRINTS; PR00024; HOMEOBOX.
KW   DNA-binding; Homeobox; Nuclear protein.
FT   NON_TER       1      1
FT   NON_TER      27     27
SQ   SEQUENCE   27 AA;  3339 MW;  9B4F2D5E657EB7F8 CRC64;

  Query Match             30.1%;  Score 28;  DB 2;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 7.7e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 NINKFL 18
              ||||:|
Db          1 NINKYL 6
```

```
RESULT 34
Q4YZJ6_PLABE
ID   Q4YZJ6_PLABE   PRELIMINARY;   PRT;    30 AA.
AC   Q4YZJ6;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Hypothetical protein (Fragment).
GN   ORFNames=PB103726.00.0;
OS   Plasmodium berghei.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5821;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15637271; DOI=10.1126/science.1103717;
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA   Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA   Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAI01001503; CAH96546.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   30 AA;  3732 MW;  EFDC5780BC5A42A9 CRC64;

  Query Match             30.1%;  Score 28;  DB 2;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 8.5e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 NINKFL 18
                ||||:|
Db          8 NINKYL 13
```

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_771_789
Perfect score: 93
Sequence: 1 SKLNESINKAMININKFLN 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	100.0	19	9	ADW11064	Adw11064 Clostridi
2	93	100.0	27	9	ADW11115	Adw11115 Clostridi
3	46	49.5	27	9	ADW11116	Adw11116 Clostridi
4	40	43.0	22	7	ADC29695	Adc29695 Antioxida
5	40	43.0	23	3	AAY89467	Aay89467 Core poly
6	40	43.0	23	3	AAY89409	Aay89409 Core poly

```
RESULT 25
ADZ15100
ID   ADZ15100 standard; peptide; 22 AA.
XX
AC   ADZ15100;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Picornavirus 2A-like NPG/P peptide #45.
XX
KW   cancer; Cytostatic; neoplasm.
XX
OS   Picornaviridae.
XX
PN   WO2005030139-A2.
XX
PD   07-APR-2005.
XX
PF   23-SEP-2004; 2004WO-US031504.
XX
PR   26-SEP-2003; 2003US-0506182P.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Hallenbeck PL,  Hay CM,  Ganesh S,  Police SR,  Xu L,  Yang J;
PI   Cheng C;
XX
DR   WPI; 2005-262902/27.
XX
PT   New Seneca Valley virus nucleic acid or polypeptide, useful in preparing
PT   a composition for treating cancer or inhibiting cancer progression.
XX
PS   Disclosure; Fig 70; 198pp; English.
XX
CC   The invention relates to a new isolated Seneca Valley virus (SVV) nucleic
CC   acid. The nucleic acid is useful in preparing a composition for treating
CC   cancer or inhibiting cancer progression. The present sequence represents
CC   the amino acid sequence of a picornavirus 2A-like NPG/P peptide.
XX
SQ   Sequence 22 AA;

  Query Match             34.3%;  Score 35;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 KFLNQC 7
              ||||||
Db          8 KFLNQC 13
```

785-803

```
RESULT 1
US-11-335-891-92
; Sequence 92, Application US/11335891
; Publication No. US20060159659A1
; GENERAL INFORMATION:
;  APPLICANT: HALLENBECK, PAUL
;  TITLE OF INVENTION: SENECA VALLEY VIRUS BASED COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  TREATING DISEASE
;  FILE REFERENCE: 287037.127US2
;  CURRENT APPLICATION NUMBER: US/11/335,891
;  CURRENT FILING DATE:  2006-01-19
;  PRIOR APPLICATION NUMBER: 60/506,182
;  PRIOR FILING DATE: 2003-09-26
;  PRIOR APPLICATION NUMBER: PCT/US2004/031504
;  PRIOR FILING DATE: 2004-09-23
;  PRIOR APPLICATION NUMBER: 60/664,442
;  PRIOR FILING DATE: 2005-03-23
;  PRIOR APPLICATION NUMBER: 60/726,313
;  PRIOR FILING DATE: 2005-10-13
;  NUMBER OF SEQ ID NOS: 227
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 92
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Ljungan virus
US-11-335-891-92

  Query Match           34.3%;  Score 35;  DB 7;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 27;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 KFLNQC 7
              ||||||
Db          8 KFLNQC 13
```

```
RESULT 28
ADZ15102
ID   ADZ15102 standard; peptide; 22 AA.
XX
AC   ADZ15102;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Picornavirus 2A-like NPG/P peptide #47.
XX
KW   cancer; Cytostatic; neoplasm.
XX
OS   Picornaviridae.
XX
PN   WO2005030139-A2.
XX
PD   07-APR-2005.
XX
PF   23-SEP-2004; 2004WO-US031504.
XX
PR   26-SEP-2003; 2003US-0506182P.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Hallenbeck PL,  Hay CM,  Ganesh S,  Police SR,  Xu L,  Yang J;
PI   Cheng C;
XX
DR   WPI; 2005-262902/27.
XX
PT   New Seneca Valley virus nucleic acid or polypeptide, useful in preparing
PT   a composition for treating cancer or inhibiting cancer progression.
XX
PS   Disclosure; Fig 70; 198pp; English.
XX
CC   The invention relates to a new isolated Seneca Valley virus (SVV) nucleic
CC   acid. The nucleic acid is useful in preparing a composition for treating
CC   cancer or inhibiting cancer progression. The present sequence represents
CC   the amino acid sequence of a picornavirus 2A-like NPG/P peptide.
XX
SQ   Sequence 22 AA;

  Query Match             34.3%;  Score 35;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 KFLNQC 7
              ||||||
Db          8 KFLNQC 13
```

RESULT 45
ADW30996
ID ADW30996 standard; peptide; 9 AA.
XX
AC ADW30996;
XX
DT 10-MAR-2005 (first entry)
XX
DE HLA binding epitope #1746.
XX
KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KW viral disease; cancer.
XX
OS Unidentified.
XX
PN WO2003040165-A2.
XX
PD 15-MAY-2003.
XX
PF 18-OCT-2001; 2001WO-US051650.
XX
PR 19-OCT-2000; 2000US-0242350P.
PR 20-APR-2001; 2001US-0285624P.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S;
XX
DR WPI; 2003-441519/41.
XX
PT New composition comprising at least one peptide having allele-specific
PT binding motifs for HLA, useful for preventing, treating or diagnosing
PT viral diseases and cancer.
XX
PS Claim 1; Page 52-379; 382pp; English.
XX
CC The invention relates to a composition comprising at least one peptide
CC having an isolated, prepared epitope selected from any of the sequences
CC from 30 lists given in the specification. Also disclosed is a method for
CC inducing a cytotoxic T cell response against a pre-selected antigen in a
CC patient expressing a specific MHC class I allele by contacting cytotoxic
CC T cells from the patient with the composition cited above. The
CC composition comprises an epitope that is joined by an amino acid linker.
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC binds to a complex of the HLA molecule and the epitope. Specifically
CC claimed are peptides having allele-specific binding motifs for HLA. The
CC compositions and methods are useful for preventing, treating or
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC diagnostic agents for evaluating immune responses, for making antibodies
CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
XX
SQ Sequence 9 AA;

  Query Match   30.4%; Score 31; DB 7; Length 9;
  Best Local Similarity   57.1%; Pred. No. 2.1e+06;
  Matches   4; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

```
Qy          13 MNSMIPY 19
               :|||::||
Db           2 LNSLVPY 8
```

```
RESULT 1
US-10-715-810-13
; Sequence 13, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 787-806)
US-10-715-810-13

  Query Match             89.2%;  Score 91;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

```
RESULT 2
US-10-715-810-28
; Sequence 28, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 350-369)
US-10-715-810-28

  Query Match             89.2%;  Score 91;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

```
RESULT 3
US-10-715-810-83
; Sequence 83, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 787-806)
US-10-715-810-83

  Query Match             89.2%;  Score 91;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
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```
RESULT 40
US-10-378-173-114
; Sequence 114, Application US/10378173
; Publication No. US20030232014A1
; GENERAL INFORMATION:
;  APPLICANT: Burke et al.
;  TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO
;  FILE REFERENCE: MDSP-P01-023
;  CURRENT APPLICATION NUMBER: US/10/378,173
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: 60/360787
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 231
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorylated peptide
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: phosphorylation
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (8)..(8)
;   OTHER INFORMATION: phosphorylation
US-10-378-173-114

  Query Match             29.4%;  Score 30;  DB 4;  Length 11;
  Best Local Similarity   55.6%;  Pred. No. 5.5e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 SYLMNSMIP 18
              :|:|||  |
Db          2 AYMMNSQSP 10
```

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_785_803
Perfect score: 102
Sequence: 1 NKFLNQCSVSYLMNSMIPY 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	19	9	ADW11065	Adw11065 Clostridi
2	102	100.0	27	9	ADW11116	Adw11116 Clostridi
3	91	89.2	20	9	ADZ69738	Adz69738 Botulinum
4	91	89.2	20	9	ADZ69808	Adz69808 Botulinum
5	91	89.2	20	9	ADZ69753	Adz69753 Botulinum
6	49	48.0	27	9	ADW11115	Adw11115 Clostridi
7	41	40.2	16	6	ABP83366	Abp83366 G protein
8	38	37.3	26	8	ABO53994	Abo53994 Human

SCORE Search Results Details for Application 10821669 and Search Result us-10-821-669-1_copy_813_831.szlm30.rup.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10821669 and Search Result us-10-821-669-1_copy_813_831.szlm30.rup.

start

Go Back to previous page

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 13:04:05 ; Search time 111.239 Seconds
(without alignments)
157.995 Million cell updates/sec

Title: US-10-821-669-1_COPY_813_831
Perfect score: 94
Sequence: 1 ASLKDALLKYIYDNRGTLI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 37017

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	42	44.7	22	2	Q4YAS5_PLABE	Q4yas5 plasmodium
2	41	43.6	26	2	Q4Y322_PLACH	Q4y322 plasmodium
3	35	37.2	28	2	P89161_SIVCZ	P89161 chimpanzee
4	34	36.2	20	2	Q9R4D2_HAEPA	Q9r4d2 haemophilus

5	32	34.0	28	2	Q4X2V6_PLACH	Q4x2v6 plasmodium
6	31	33.0	21	2	O25621_HELPY	O25621 helicobacte
7	31	33.0	23	2	Q4Z2T5_PLABE	Q4z2t5 plasmodium
8	31	33.0	25	2	Q4YGW4_PLABE	Q4ygw4 plasmodium
9	31	33.0	27	2	Q4X7E7_PLACH	Q4x7e7 plasmodium
10	31	33.0	27	2	Q4XIW2_PLACH	Q4xiw2 plasmodium
11	31	33.0	29	2	Q57I38_SALCH	Q57i38 salmonella
12	31	33.0	29	2	Q8ZL14_SALTY	Q8zl14 salmonella
13	31	33.0	30	2	Q4YJP6_PLABE	Q4yjp6 plasmodium
14	30	31.9	21	1	OMP1_HAEPR	P80369 haemophilus
15	30	31.9	26	2	Q4RDE7_TETNG	Q4rde7 tetraodon n
16	30	31.9	29	2	O62784_ISOMA	O62784 isoodon mac
17	29	30.9	17	2	Q9QV51_9MURI	Q9qv51 mus sp. 60
18	29	30.9	20	1	OMPH_HAEGA	P80451 haemophilus
19	28	29.8	10	2	Q9PRU1_CYNPY	Q9pru1 cynops pyrr
20	28	29.8	13	2	Q6TKR2_HUMAN	Q6tkr2 homo sapien
21	28	29.8	22	2	Q96Q57_HUMAN	Q96q57 homo sapien
22	28	29.8	23	2	Q7RLB8_PLAYO	Q7rlb8 plasmodium
23	28	29.8	24	2	Q4XDJ9_PLACH	Q4xdj9 plasmodium
24	28	29.8	24	2	Q9R5S1_ENTHR	Q9r5s1 enterococcu
25	28	29.8	25	2	Q56CB0_9HIV1	Q56cb0 human immun
26	28	29.8	26	2	Q6EML2_MELGA	Q6eml2 meleagris g
27	28	29.8	26	2	Q6EML3_CHICK	Q6eml3 gallus gall
28	28	29.8	27	2	Q6U210_HUMAN	Q6u210 homo sapien
29	28	29.8	27	2	Q4X644_PLACH	Q4x644 plasmodium
30	28	29.8	30	2	Q4YER7_PLABE	Q4yer7 plasmodium
31	27.5	29.3	30	2	Q4Y299_PLACH	Q4y299 plasmodium
32	27	28.7	19	2	Q53502_LACPA	Q53502 lactobacill
33	27	28.7	20	1	PEPT_FUSNP	P81207 fusobacteri
34	27	28.7	20	2	Q4XVG2_PLACH	Q4xvg2 plasmodium
35	27	28.7	20	2	Q4YMR5_PLABE	Q4ymr5 plasmodium
36	27	28.7	20	2	Q9PS63_CHICK	Q9ps63 gallus gall
37	27	28.7	22	1	OMPH_PASGA	P80454 pasteurella
38	27	28.7	22	1	OMPH_PASVO	P80452 pasteurella
39	27	28.7	23	2	Q8MFJ9_9FILI	Q8mfj9 hymenophyll
40	27	28.7	23	2	Q8MFK5_9FILI	Q8mfk5 hymenophyll
41	27	28.7	24	2	Q4X3E2_PLACH	Q4x3e2 plasmodium
42	27	28.7	24	2	Q4Y887_PLACH	Q4y887 plasmodium
43	27	28.7	26	1	PSAE_SYNVU	P20900 synechococc
44	27	28.7	26	2	Q4XR84_PLACH	Q4xr84 plasmodium
45	27	28.7	28	2	Q4YGQ5_PLABE	Q4ygq5 plasmodium
46	27	28.7	28	2	Q7R7G7_PLAYO	Q7r7g7 plasmodium
47	27	28.7	29	2	Q4X4G9_PLACH	Q4x4g9 plasmodium
48	27	28.7	29	2	Q4Y032_PLACH	Q4y032 plasmodium
49	27	28.7	29	2	Q4YBJ7_PLABE	Q4ybj7 plasmodium
50	27	28.7	30	2	Q4XEF3_PLACH	Q4xef3 plasmodium
51	27	28.7	30	2	Q7RGP6_PLAYO	Q7rgp6 plasmodium
52	27	28.7	30	2	Q65TQ7_MANSM	Q65tq7 mannheimia
53	26.5	28.2	20	2	Q63667_RAT	Q63667 rattus norv
54	26.5	28.2	23	2	Q5H797_9NEOP	Q5h797 hodotermops
55	26	27.7	15	2	Q70Y59_ROSOF	Q70y59 rosmarinus
56	26	27.7	15	2	Q9R4K9_SPIME	Q9r4k9 spiroplasma
57	26	27.7	19	2	Q9BVX6_HUMAN	Q9bvx6 homo sapien
58	26	27.7	19	2	Q4XUW5_PLACH	Q4xuw5 plasmodium
59	26	27.7	19	2	Q4XZW1_PLACH	Q4xzw1 plasmodium
60	26	27.7	19	2	Q70Y73_9LAMI	Q70y73 pycnostachy
61	26	27.7	20	2	Q9TRM7_BOVIN	Q9trm7 bos taurus
62	26	27.7	20	2	Q9R5E3_AERHY	Q9r5e3 aeromonas h
63	26	27.7	21	1	OMP1_ACTEU	P80443 actinobacil
64	26	27.7	21	1	OMP1_ACTPL	P80368 actinobacil
65	26	27.7	21	1	OMP1_ACTSU	P80442 actinobacil

66	26	27.7	22	2	Q4YG47_PLABE	Q4yg47 plasmodium
67	26	27.7	22	2	Q9TC82_CENEN	Q9tc82 centropomus
68	26	27.7	22	2	Q9TC84_9PERO	Q9tc84 centropomus
69	26	27.7	23	2	Q4XH19_PLACH	Q4xh19 plasmodium
70	26	27.7	23	2	Q4Y4S8_PLACH	Q4y4s8 plasmodium
71	26	27.7	24	2	Q4XS89_PLACH	Q4xs89 plasmodium
72	26	27.7	25	2	Q4YSL4_PLABE	Q4ysl4 plasmodium
73	26	27.7	26	2	Q684V1_9SCOR	Q684v1 mesobuthus
74	26	27.7	27	2	Q06699_YEAST	Q06699 saccharomyc
75	26	27.7	27	2	Q4YHV3_PLABE	Q4yhv3 plasmodium
76	26	27.7	28	2	Q4XCS0_PLACH	Q4xcs0 plasmodium
77	26	27.7	28	2	Q4XFN5_PLACH	Q4xfn5 plasmodium
78	26	27.7	28	2	Q4XR83_PLACH	Q4xr83 plasmodium
79	26	27.7	28	2	Q4YBP0_PLABE	Q4ybp0 plasmodium
80	26	27.7	28	2	Q4YEZ4_PLABE	Q4yez4 plasmodium
81	26	27.7	28	2	Q5G7D5_9HIV1	Q5g7d5 human immun
82	26	27.7	29	1	ATPA_BRYMA	P26965 bryopsis ma
83	26	27.7	29	2	Q46303_CLOPE	Q46303 clostridium
84	26	27.7	29	2	Q8CJ37_MOUSE	Q8cj37 mus musculu
85	26	27.7	30	2	Q7RT29_PLAYO	Q7rt29 plasmodium
86	26	27.7	30	2	Q7M313_PIG	Q7m313 sus scrofa
87	26	27.7	30	2	Q3D251_STRAG	Q3d251 streptococc
88	26	27.7	30	2	Q3DNJ4_STRAG	Q3dnj4 streptococc
89	26	27.7	30	2	Q4MN89_BACCE	Q4mn89 bacillus ce
90	26	27.7	30	2	Q2NCJ0_9SPHN	Q2ncj0 erythrobact
91	26	27.7	30	2	Q57CL6_BRUAB	Q57cl6 brucella ab
92	26	27.7	30	2	Q2YRG2_BRUA2	Q2yrg2 brucella ab
93	25.5	27.1	22	2	Q4Y4T1_PLACH	Q4y4t1 plasmodium
94	25.5	27.1	30	1	Y357_BORBU	O51332 borrelia bu
95	25	26.6	16	2	Q90XT4_PHORB	Q90xt4 phoenicopte
96	25	26.6	18	2	Q53BU2_SCYSP	Q53bu2 scytalopus
97	25	26.6	18	2	Q53BU3_9PASS	Q53bu3 pteroptocho
98	25	26.6	18	2	Q53BU4_9PASS	Q53bu4 chamaeza me
99	25	26.6	18	2	Q53BU5_9DEND	Q53bu5 xiphorhynch
100	25	26.6	18	2	Q53BU6_9DEND	Q53bu6 xiphocolapt
101	25	26.6	18	2	Q53BU7_9DEND	Q53bu7 sittasomus
102	25	26.6	18	2	Q53BU8_9FURN	Q53bu8 nasica long
103	25	26.6	18	2	Q53BU9_9DEND	Q53bu9 xiphorhynch
104	25	26.6	18	2	Q53BV0_9FURN	Q53bv0 glyphorynch
105	25	26.6	18	2	Q53BV1_9DEND	Q53bv1 drymornis b
106	25	26.6	18	2	Q53BV2_9DEND	Q53bv2 dendrocincl
107	25	26.6	18	2	Q53BV4_9DEND	Q53bv4 campylorham
108	25	26.6	18	2	Q53BV5_9FURN	Q53bv5 pygarrhicha
109	25	26.6	18	2	Q53BV6_9FURN	Q53bv6 xenops ruti
110	25	26.6	18	2	Q53BV7_9FURN	Q53bv7 xenops minu
111	25	26.6	18	2	Q53BV8_9FURN	Q53bv8 lochmias ne
112	25	26.6	18	2	Q53BV9_9FURN	Q53bv9 sclerurus s
113	25	26.6	18	2	Q53BW0_9FURN	Q53bw0 sclerurus m
114	25	26.6	18	2	Q53BW1_9FURN	Q53bw1 automolus l
115	25	26.6	18	2	Q53BW2_9FURN	Q53bw2 thripadecte
116	25	26.6	18	2	Q53BW3_9FURN	Q53bw3 philydor at
117	25	26.6	18	2	Q53BW4_9FURN	Q53bw4 berlepschia
118	25	26.6	18	2	Q53BW5_9FURN	Q53bw5 margarornis
119	25	26.6	18	2	Q53BW6_9FURN	Q53bw6 coryphister
120	25	26.6	18	2	Q53BW7_9FURN	Q53bw7 anumbius an
121	25	26.6	18	2	Q53BW8_9FURN	Q53bw8 phacellodom
122	25	26.6	18	2	Q53BW9_9FURN	Q53bw9 asthenes ca
123	25	26.6	18	2	Q53BX0_9FURN	Q53bx0 cranioleuca
124	25	26.6	18	2	Q53BX2_9FURN	Q53bx2 leptasthenu
125	25	26.6	18	2	Q53BX3_9FURN	Q53bx3 furnarius c
126	25	26.6	18	2	Q53BX4_9FURN	Q53bx4 cinclodes f

127	25	26.6	18	2	Q53BX5_9FURN	Q53bx5 upucerthia
128	25	26.6	18	2	Q53BX7_9FURN	Q53bx7 geositta ru
129	25	26.6	18	2	Q5XMF3_9AVES	Q5xmf3 oxyura macc
130	25	26.6	18	2	Q5XMF4_9AVES	Q5xmf4 oxyura aust
131	25	26.6	18	2	Q5XMF5_OXYJA	Q5xmf5 oxyura jama
132	25	26.6	18	2	Q5XMF6_OXYVI	Q5xmf6 oxyura vitt
133	25	26.6	18	2	Q5XMF7_9AVES	Q5xmf7 nomonyx dom
134	25	26.6	18	2	Q68LC1_9PASS	Q68lc1 phaenostict
135	25	26.6	18	2	Q68LC2_9PASS	Q68lc2 rhegmatorhi
136	25	26.6	18	2	Q68LC3_9PASS	Q68lc3 gymnopithys
137	25	26.6	18	2	Q68LC4_9PASS	Q68lc4 pithys albi
138	25	26.6	18	2	Q68LC5_9PASS	Q68lc5 myrmornis t
139	25	26.6	18	2	Q68LC6_9PASS	Q68lc6 gymnocichla
140	25	26.6	18	2	Q68LC8_9PASS	Q68lc8 myrmeciza f
141	25	26.6	18	2	Q68LC9_9PASS	Q68lc9 myrmeciza l
142	25	26.6	18	2	Q68LD0_9PASS	Q68ld0 myrmeciza h
143	25	26.6	18	2	Q68LD1_9PASS	Q68ld1 myrmeciza g
144	25	26.6	18	2	Q68LD2_9PASS	Q68ld2 schistocich
145	25	26.6	18	2	Q68LD3_9PASS	Q68ld3 sclateria n
146	25	26.6	18	2	Q68LD4_9PASS	Q68ld4 hypocnemoid
147	25	26.6	18	2	Q68LD5_9PASS	Q68ld5 myrmochanes
148	25	26.6	18	2	Q68LD6_9PASS	Q68ld6 hypocnemis
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150	25	26.6	18	2	Q68LD8_9PASS	Q68ld8 myrmoborus
151	25	26.6	18	2	Q68LD9_9PASS	Q68ld9 neoctantes
152	25	26.6	18	2	Q68LE1_9PASS	Q68le1 cercomacra
153	25	26.6	18	2	Q68LE2_9PASS	Q68le2 myrmorchilu
154	25	26.6	18	2	Q68LE3_9PASS	Q68le3 formicivora
155	25	26.6	18	2	Q68LE4_9PASS	Q68le4 drymophila
156	25	26.6	18	2	Q68LE5_9PASS	Q68le5 terenura hu
157	25	26.6	18	2	Q68LE6_9PASS	Q68le6 myrmotherul
158	25	26.6	18	2	Q68LE7_9PASS	Q68le7 myrmotherul
159	25	26.6	18	2	Q68LE8_MYRAX	Q68le8 myrmotherul
160	25	26.6	18	2	Q68LF0_MYRLE	Q68lf0 myrmotherul
161	25	26.6	18	2	Q68LF2_9PASS	Q68lf2 microrhopia
162	25	26.6	18	2	Q68LF3_9PASS	Q68lf3 herpsilochm
163	25	26.6	18	2	Q68LF4_9PASS	Q68lf4 dysithamnus
164	25	26.6	18	2	Q68LF5_9PASS	Q68lf5 thamnomanes
165	25	26.6	18	2	Q68LF6_9PASS	Q68lf6 thamnistes
166	25	26.6	18	2	Q68LF7_9PASS	Q68lf7 pygiptila s
167	25	26.6	18	2	Q68LF8_9PASS	Q68lf8 megastictus
168	25	26.6	18	2	Q68LF9_9PASS	Q68lf9 thamnophilu
169	25	26.6	18	2	Q68LG0_9PASS	Q68lg0 thamnophilu
170	25	26.6	18	2	Q68LG1_9PASS	Q68lg1 thamnophilu
171	25	26.6	18	2	Q68LG2_9PASS	Q68lg2 thamnophilu
172	25	26.6	18	2	Q68LG4_9PASS	Q68lg4 taraba majo
173	25	26.6	18	2	Q68LG5_9PASS	Q68lg5 batara cine
174	25	26.6	18	2	Q68LG6_9PASS	Q68lg6 hypoedaleus
175	25	26.6	18	2	Q68LG7_9PASS	Q68lg7 mackenziaen
176	25	26.6	18	2	Q68LG8_9PASS	Q68lg8 fredericken
177	25	26.6	18	2	Q6UQQ7_9PASE	Q6uqq7 anomalospiz
178	25	26.6	18	2	Q6UQQ8_9PASS	Q6uqq8 vidua orien
179	25	26.6	18	2	Q6UQQ9_9PASS	Q6uqq9 vidua obtus
180	25	26.6	18	2	Q6UQR0_9PASS	Q6uqr0 vidua hypoc
181	25	26.6	18	2	Q6UQR2_9PASS	Q6uqr2 vidua macro
182	25	26.6	18	2	Q6UQR3_9PASS	Q6uqr3 vidua wilso
183	25	26.6	18	2	Q6UQR4_9PASS	Q6uqr4 vidua camer
184	25	26.6	18	2	Q6UQR5_9PASS	Q6uqr5 vidua raric
185	25	26.6	18	2	Q6UQR6_9PASS	Q6uqr6 vidua regia
186	25	26.6	18	2	Q6UQR7_9PASS	Q6uqr7 vidua fisch
187	25	26.6	18	2	Q90XS9_ANAPL	Q90xs9 anas platyr

188	25	26.6	18	2	Q90XT1_9CHAR	Q90xt1 charadrius
189	25	26.6	18	2	Q90XT3_9AVES	Q90xt3 aechmophoru
190	25	26.6	18	2	Q90XT6_GAVST	Q90xt6 gavia stell
191	25	26.6	18	2	Q90XT7_PYGAD	Q90xt7 pygoscelis
192	25	26.6	18	2	Q90XT8_CICNG	Q90xt8 ciconia nig
193	25	26.6	18	2	Q90XT9_NYCNY	Q90xt9 nycticorax
194	25	26.6	18	2	Q90XU5_9AVES	Q90xu5 sula neboux
195	25	26.6	18	2	Q90XU6_9AVES	Q90xu6 phaethon ae
196	25	26.6	18	2	Q68LC7_MYRBR	Q68lc7 myrmeciza b
197	25	26.6	19	2	Q6Y078_9PSIT	Q6y078 amazona ama
198	25	26.6	19	2	Q6Y080_9PSIT	Q6y080 amazona och
199	25	26.6	19	2	Q6Y081_9PSIT	Q6y081 amazona och
200	25	26.6	19	2	Q6Y082_9PSIT	Q6y082 amazona och
201	25	26.6	20	2	Q6LDX5_HUMAN	Q6ldx5 homo sapien
202	25	26.6	20	2	Q7LZU6_9INFA	Q7lzu6 influenza a
203	25	26.6	21	2	Q87575_SIVCZ	Q87575 chimpanzee
204	25	26.6	21	2	Q87585_SIVCZ	Q87585 chimpanzee
205	25	26.6	22	2	Q4XC36_PLACH	Q4xc36 plasmodium
206	25	26.6	22	2	Q4Z392_PLABE	Q4z392 plasmodium
207	25	26.6	22	2	Q4Z5M8_PLABE	Q4z5m8 plasmodium
208	25	26.6	22	2	Q9QWB6_9MURI	Q9qwb6 mus sp. sgp
209	25	26.6	23	2	Q4Y4S6_PLACH	Q4y4s6 plasmodium
210	25	26.6	24	2	Q4Z0G6_PLABE	Q4z0g6 plasmodium
211	25	26.6	25	2	Q4XD90_PLACH	Q4xd90 plasmodium
212	25	26.6	25	2	Q4YG46_PLABE	Q4yg46 plasmodium
213	25	26.6	25	2	Q6YJ06_9RHOD	Q6yj06 porphyra ra
214	25	26.6	25	2	O26056_HELPY	O26056 helicobacte
215	25	26.6	25	2	Q3S9W7_9HIV1	Q3s9w7 human immun
216	25	26.6	26	1	ACHD_ELEEL	P09691 electrophor
217	25	26.6	26	2	Q91U56_9INFA	Q91u56 influenza a
218	25	26.6	27	2	Q4X3J6_PLACH	Q4x3j6 plasmodium
219	25	26.6	27	2	Q4X3K5_PLACH	Q4x3k5 plasmodium
220	25	26.6	27	2	Q4XAJ2_PLACH	Q4xaj2 plasmodium
221	25	26.6	27	2	Q4XHN8_PLACH	Q4xhn8 plasmodium
222	25	26.6	27	2	Q4XI91_PLACH	Q4xi91 plasmodium
223	25	26.6	27	2	Q4XSN8_PLACH	Q4xsn8 plasmodium
224	25	26.6	27	2	Q6V7V8_CHICK	Q6v7v8 gallus gall
225	25	26.6	28	2	Q4X7K6_PLACH	Q4x7k6 plasmodium
226	25	26.6	28	2	Q4YMK5_PLABE	Q4ymk5 plasmodium
227	25	26.6	29	1	PLMS_SCYCA	P83650 scyliorhinu
228	25	26.6	29	2	Q4XJX6_PLACH	Q4xjx6 plasmodium
229	25	26.6	29	2	Q4XSZ6_PLACH	Q4xsz6 plasmodium
230	25	26.6	29	2	Q6JDN0_CANFA	Q6jdn0 canis famil
231	25	26.6	29	2	Q3CYH8_STRAG	Q3cyh8 streptococc
232	25	26.6	29	2	Q4TF38_TETNG	Q4tf38 tetraodon n
233	25	26.6	30	2	Q35904_SCHPO	Q35904 schizosacch
234	25	26.6	30	2	Q7RJB8_PLAYO	Q7rjb8 plasmodium
235	25	26.6	30	2	Q84JV1_CRYJA	Q84jv1 cryptomeria
236	25	26.6	30	2	Q4SAM1_TETNG	Q4sam1 tetraodon n
237	24.5	26.1	21	2	Q9F7Y5_NEIGO	Q9f7y5 neisseria g
238	24.5	26.1	29	2	O03120_9EMBR	O03120 megaceros v
239	24.5	26.1	29	2	Q7A5V9_STAAN	Q7a5v9 staphylococ
240	24.5	26.1	29	2	Q8NWX8_STAAW	Q8nwx8 staphylococ
241	24.5	26.1	29	2	Q99UH5_STAAM	Q99uh5 staphylococ
242	24.5	26.1	30	2	Q6MKG8_BDEBA	Q6mkg8 bdellovibri
243	24	25.5	14	2	Q4JHP1_9CARY	Q4jhp1 suaeda liao
244	24	25.5	14	2	Q70Y61_9LAMI	Q70y61 ocimum sell
245	24	25.5	14	2	Q6R7V0_9SAUR	Q6r7v0 carlia viva
246	24	25.5	15	2	Q9S8P1_RAPSA	Q9s8p1 raphanus sa
247	24	25.5	16	2	Q6Y079_AMAAE	Q6y079 amazona aes
248	24	25.5	17	2	Q7XB06_MAIZE	Q7xb06 zea mays (m

249	24	25.5	17	2	Q4VI71_9SAUR	Q4vi71 actinemys m
250	24	25.5	17	2	Q6R7U8_9SAUR	Q6r7u8 lampropholi
251	24	25.5	17	2	Q6R7U9_9SAUR	Q6r7u9 saproscincu
252	24	25.5	17	2	Q6R7V1_9SAUR	Q6r7v1 carlia rost
253	24	25.5	17	2	Q6R7V2_9SAUR	Q6r7v2 carlia rufi
254	24	25.5	17	2	Q6R7V3_9SAUR	Q6r7v3 carlia fusc
255	24	25.5	17	2	Q6R7V5_9SAUR	Q6r7v5 carlia rhom
256	24	25.5	17	2	Q6R7V6_9SAUR	Q6r7v6 carlia rubr
257	24	25.5	18	2	Q7Y4F7_9CAUD	Q7y4f7 lactococcus
258	24	25.5	18	2	Q7Y4G1_9CAUD	Q7y4g1 lactococcus
259	24	25.5	18	2	Q7XB07_MAIZE	Q7xb07 zea mays (m
260	24	25.5	18	2	Q2PDK6_CLODI	Q2pdk6 clostridium
261	24	25.5	18	2	Q9PXB6_ADE05	Q9pxb6 human adeno
262	24	25.5	18	2	Q53BV3_9FURN	Q53bv3 deconychura
263	24	25.5	18	2	Q53BX6_9FURN	Q53bx6 geositta te
264	24	25.5	19	2	Q8IVH1_HUMAN	Q8ivh1 homo sapien
265	24	25.5	19	2	Q70Y92_9LAMI	Q70y92 platostoma
266	24	25.5	20	2	Q4XCZ2_PLACH	Q4xcz2 plasmodium
267	24	25.5	20	2	Q4A2D6_9PHYC	Q4a2d6 emiliania h
268	24	25.5	21	2	Q4Y8T8_PLACH	Q4y8t8 plasmodium
269	24	25.5	21	2	Q4YDB9_PLABE	Q4ydb9 plasmodium
270	24	25.5	21	2	Q4YTM1_PLABE	Q4ytm1 plasmodium
271	24	25.5	21	2	Q9RQ26_CLODI	Q9rq26 clostridium
272	24	25.5	22	2	Q6BGN9_DEBHA	Q6bgn9 debaryomyce
273	24	25.5	22	2	Q4X8D6_PLACH	Q4x8d6 plasmodium
274	24	25.5	22	2	Q4YMD8_PLABE	Q4ymd8 plasmodium
275	24	25.5	22	2	Q9MX47_ORYLA	Q9mx47 oryzias lat
276	24	25.5	23	2	Q9UCE3_HUMAN	Q9uce3 homo sapien
277	24	25.5	23	2	Q4YG20_PLABE	Q4yg20 plasmodium
278	24	25.5	23	2	Q5XYL3_BORGA	Q5xyl3 borrelia ga
279	24	25.5	23	2	Q6UK03_VIBCH	Q6uk03 vibrio chol
280	24	25.5	24	2	Q4X4X8_PLACH	Q4x4x8 plasmodium
281	24	25.5	24	2	Q4XCF4_PLACH	Q4xcf4 plasmodium
282	24	25.5	24	2	Q4XY90_PLACH	Q4xy90 plasmodium
283	24	25.5	24	2	Q7RDJ7_PLAYO	Q7rdj7 plasmodium
284	24	25.5	24	2	Q46081_CLOHU	Q46081 clostridium
285	24	25.5	25	1	TFDC1_COMAC	P83115 comamonas a
286	24	25.5	25	2	Q4XMQ2_PLACH	Q4xmq2 plasmodium
287	24	25.5	25	2	Q4Y1J7_PLACH	Q4y1j7 plasmodium
288	24	25.5	25	2	Q4YT11_PLABE	Q4yt11 plasmodium
289	24	25.5	25	2	Q9N150_BOVIN	Q9n150 bos taurus
290	24	25.5	25	2	O49748_ARATH	O49748 arabidopsis
291	24	25.5	25	2	Q56C92_9HIV1	Q56c92 human immun
292	24	25.5	25	2	Q56CA1_9HIV1	Q56ca1 human immun
293	24	25.5	25	2	Q56CA7_9HIV1	Q56ca7 human immun
294	24	25.5	25	2	Q56CA8_9HIV1	Q56ca8 human immun
295	24	25.5	25	2	Q56CB5_9HIV1	Q56cb5 human immun
296	24	25.5	25	2	Q56CB7_9HIV1	Q56cb7 human immun
297	24	25.5	25	2	Q56CB8_9HIV1	Q56cb8 human immun
298	24	25.5	25	2	Q56CB9_9HIV1	Q56cb9 human immun
299	24	25.5	25	2	Q56CC0_9HIV1	Q56cc0 human immun
300	24	25.5	25	2	Q56CC1_9HIV1	Q56cc1 human immun
301	24	25.5	25	2	Q56CC2_9HIV1	Q56cc2 human immun
302	24	25.5	25	2	Q56CC3_9HIV1	Q56cc3 human immun
303	24	25.5	25	2	Q56CC4_9HIV1	Q56cc4 human immun
304	24	25.5	25	2	Q56CC5_9HIV1	Q56cc5 human immun
305	24	25.5	25	2	Q56CC6_9HIV1	Q56cc6 human immun
306	24	25.5	25	2	Q56CC7_9HIV1	Q56cc7 human immun
307	24	25.5	25	2	Q56CC8_9HIV1	Q56cc8 human immun
308	24	25.5	25	2	Q56CC9_9HIV1	Q56cc9 human immun
309	24	25.5	25	2	Q56CD1_9HIV1	Q56cd1 human immun

310	24	25.5	25	2	Q56CD2_9HIV1	Q56cd2 human immun
311	24	25.5	25	2	Q56CD3_9HIV1	Q56cd3 human immun
312	24	25.5	25	2	Q56CD4_9HIV1	Q56cd4 human immun
313	24	25.5	25	2	Q56CD5_9HIV1	Q56cd5 human immun
314	24	25.5	25	2	Q56CD6_9HIV1	Q56cd6 human immun
315	24	25.5	25	2	Q56CD7_9HIV1	Q56cd7 human immun
316	24	25.5	25	2	Q56CD8_9HIV1	Q56cd8 human immun
317	24	25.5	25	2	Q56CD9_9HIV1	Q56cd9 human immun
318	24	25.5	25	2	Q56CE0_9HIV1	Q56ce0 human immun
319	24	25.5	25	2	Q56CE1_9HIV1	Q56ce1 human immun
320	24	25.5	25	2	Q56CE2_9HIV1	Q56ce2 human immun
321	24	25.5	25	2	Q56CE3_9HIV1	Q56ce3 human immun
322	24	25.5	25	2	Q56CE4_9HIV1	Q56ce4 human immun
323	24	25.5	25	2	Q56CE5_9HIV1	Q56ce5 human immun
324	24	25.5	25	2	Q56CE6_9HIV1	Q56ce6 human immun
325	24	25.5	25	2	Q56CE7_9HIV1	Q56ce7 human immun
326	24	25.5	25	2	Q56CE8_9HIV1	Q56ce8 human immun
327	24	25.5	25	2	Q56CE9_9HIV1	Q56ce9 human immun
328	24	25.5	25	2	Q56CF0_9HIV1	Q56cf0 human immun
329	24	25.5	25	2	Q56CF1_9HIV1	Q56cf1 human immun
330	24	25.5	25	2	Q56CF2_9HIV1	Q56cf2 human immun
331	24	25.5	25	2	Q56CF3_9HIV1	Q56cf3 human immun
332	24	25.5	25	2	Q56CF4_9HIV1	Q56cf4 human immun
333	24	25.5	25	2	Q58Q98_9HIV1	Q58q98 human immun
334	24	25.5	25	2	Q58QA5_9HIV1	Q58qa5 human immun
335	24	25.5	25	2	Q71969_9HIV1	Q71969 human immun
336	24	25.5	25	2	Q71988_9HIV1	Q71988 human immun
337	24	25.5	25	2	Q71994_9HIV1	Q71994 human immun
338	24	25.5	25	2	Q72010_9HIV1	Q72010 human immun
339	24	25.5	25	2	Q72016_9HIV1	Q72016 human immun
340	24	25.5	25	2	Q72020_9HIV1	Q72020 human immun
341	24	25.5	25	2	Q80273_9HIV1	Q80273 human immun
342	24	25.5	25	2	Q8QDX7_9HIV1	Q8qdx7 human immun
343	24	25.5	25	2	Q8QDY1_9HIV1	Q8qdy1 human immun
344	24	25.5	25	2	Q9IQP7_9HIV1	Q9iqp7 human immun
345	24	25.5	25	2	Q9IQQ7_9HIV1	Q9iqq7 human immun
346	24	25.5	25	2	Q9IQQ8_9HIV1	Q9iqq8 human immun
347	24	25.5	25	2	Q9IQQ9_9HIV1	Q9iqq9 human immun
348	24	25.5	25	2	Q9IQR0_9HIV1	Q9iqr0 human immun
349	24	25.5	25	2	Q9IQR1_9HIV1	Q9iqr1 human immun
350	24	25.5	26	2	Q4YJN2_PLABE	Q4yjn2 plasmodium
351	24	25.5	26	2	Q4YQR4_PLABE	Q4yqr4 plasmodium
352	24	25.5	26	2	Q7R9B5_PLAYO	Q7r9b5 plasmodium
353	24	25.5	26	2	Q7X642_MAIZE	Q7x642 zea mays (m
354	24	25.5	26	2	O86138_CLOBU	O86138 clostridium
355	24	25.5	26	2	Q7B304_CLOBU	Q7b304 clostridium
356	24	25.5	26	2	Q4RA30_TETNG	Q4ra30 tetraodon n
357	24	25.5	26	2	Q4PU49_9HIV1	Q4pu49 human immun
358	24	25.5	26	2	Q4PU54_9HIV1	Q4pu54 human immun
359	24	25.5	26	2	Q4PU59_9HIV1	Q4pu59 human immun
360	24	25.5	27	1	HCY5_HOMAM	P82300 homarus ame
361	24	25.5	27	1	KT395_PICKL	P80326 pichia kluy
362	24	25.5	27	2	Q6YJ05_9RHOD	Q6yj05 porphyra ra
363	24	25.5	27	2	Q7X644_MAIZE	Q7x644 zea mays (m
364	24	25.5	27	2	Q6V7G9_VIBCH	Q6v7g9 vibrio chol
365	24	25.5	28	2	Q4X2X3_PLACH	Q4x2x3 plasmodium
366	24	25.5	28	2	Q4X4G5_PLACH	Q4x4g5 plasmodium
367	24	25.5	28	2	Q4YRV9_PLABE	Q4yrv9 plasmodium
368	24	25.5	28	2	Q4G226_COLGU	Q4g226 colobus gue
369	24	25.5	28	2	Q7XB04_MAIZE	Q7xb04 zea mays (m
370	24	25.5	28	2	Q9R4Z2_LACAC	Q9r4z2 lactobacill

371	24	25.5	29	2	O44023_PARTE	O44023 paramecium
372	24	25.5	29	2	Q5BYX3_SCHJA	Q5byx3 schistosoma
373	24	25.5	29	2	Q56XC2_ARATH	Q56xc2 arabidopsis
374	24	25.5	29	2	Q7X643_MAIZE	Q7x643 zea mays (m
375	24	25.5	30	2	Q25627_ONCVO	Q25627 onchocerca
376	24	25.5	30	2	Q4XG67_PLACH	Q4xg67 plasmodium
377	24	25.5	30	2	Q4XT96_PLACH	Q4xt96 plasmodium
378	24	25.5	30	2	Q4Y4P6_PLACH	Q4y4p6 plasmodium
379	24	25.5	30	2	Q4Z577_PLABE	Q4z577 plasmodium
380	24	25.5	30	2	Q3ACN1_CARHZ	Q3acn1 carboxydoth
381	24	25.5	30	2	Q3DPB2_STRAG	Q3dpb2 streptococc
382	24	25.5	30	2	Q44EF2_CHRSL	Q44ef2 chromohalob
383	24	25.5	30	2	Q4MSY5_BACCE	Q4msy5 bacillus ce
384	24	25.5	30	2	Q314V3_DESDG	Q314v3 desulfovibr
385	24	25.5	30	2	Q7MVC5_PORGI	Q7mvc5 porphyromon
386	24	25.5	30	2	Q8EH33_SHEON	Q8eh33 shewanella
387	23.5	25.0	20	2	Q9S8X5_SOYBN	Q9s8x5 glycine max
388	23.5	25.0	22	2	Q9URC2_PHACH	Q9urc2 phanerochae
389	23.5	25.0	22	2	Q9URC3_PHACH	Q9urc3 phanerochae
390	23.5	25.0	23	2	Q4XPS0_PLACH	Q4xps0 plasmodium
391	23.5	25.0	26	2	Q4YLV0_PLABE	Q4ylv0 plasmodium
392	23.5	25.0	26	2	Q9IDW1_9HIV2	Q9idw1 human immun
393	23.5	25.0	27	2	Q4XG60_PLACH	Q4xg60 plasmodium
394	23.5	25.0	28	2	Q4YEQ5_PLABE	Q4yeq5 plasmodium
395	23.5	25.0	28	2	Q9XGE6_VICFA	Q9xge6 vicia faba
396	23	24.5	8	2	Q6EX61_9LAMI	Q6ex61 isodon hisp
397	23	24.5	10	1	SC46_TITCA	P84686 tityus camb
398	23	24.5	10	2	Q947R7_SOLTU	Q947r7 solanum tub
399	23	24.5	12	2	Q70Y67_9LAMI	Q70y67 prostanther
400	23	24.5	12	2	Q8GSB9_LOLPR	Q8gsb9 lolium pere
401	23	24.5	14	2	Q70Y96_9LAMI	Q70y96 ocimum amer
402	23	24.5	14	2	Q9ZRS3_ARATH	Q9zrs3 arabidopsis
403	23	24.5	15	2	Q88954_9POXV	Q88954 vaccinia vi
404	23	24.5	16	1	UVSX_BPT6	Q06728 bacteriopha
405	23	24.5	16	2	Q51950_9ZZZZ	Q51950 plasmid pns
406	23	24.5	16	2	Q9R5E9_HAESO	Q9r5e9 haemophilus
407	23	24.5	16	2	Q5DUA1_STALE	Q5dua1 staphylococ
408	23	24.5	17	1	BOL4_MEGPE	P07495 megabombus
409	23	24.5	17	2	Q4YDE5_PLABE	Q4yde5 plasmodium
410	23	24.5	17	2	Q70Y62_MENSU	Q70y62 mentha suav
411	23	24.5	17	2	Q9T2H6_SPIOL	Q9t2h6 spinacia ol
412	23	24.5	17	2	Q712C7_RHIME	Q712c7 rhizobium m
413	23	24.5	18	2	Q7SCI4_NEUCR	Q7sci4 neurospora
414	23	24.5	18	2	Q4XSK3_PLACH	Q4xsk3 plasmodium
415	23	24.5	18	2	Q6ZYV2_9CARY	Q6zyv2 silene oste
416	23	24.5	19	2	Q45SP2_CLODI	Q45sp2 clostridium
417	23	24.5	20	1	JHBP_BOMMO	P81627 bombyx mori
418	23	24.5	20	1	NF03_NAEFO	P83898 naegleria f
419	23	24.5	20	2	Q7SAL6_NEUCR	Q7sal6 neurospora
420	23	24.5	21	2	Q4XF50_PLACH	Q4xf50 plasmodium
421	23	24.5	21	2	Q4Y571_PLACH	Q4y571 plasmodium
422	23	24.5	21	2	Q7RBF8_PLAYO	Q7rbf8 plasmodium
423	23	24.5	21	2	Q9ESX0_MOUSE	Q9esx0 mus musculu
424	23	24.5	21	2	O11791_9HIV1	O11791 human immun
425	23	24.5	21	2	O11803_9HIV1	O11803 human immun
426	23	24.5	21	2	O11804_9HIV1	O11804 human immun
427	23	24.5	21	2	O11806_9HIV1	O11806 human immun
428	23	24.5	21	2	O11807_9HIV1	O11807 human immun
429	23	24.5	21	2	O11812_9HIV1	O11812 human immun
430	23	24.5	21	2	O11825_9HIV1	O11825 human immun
431	23	24.5	21	2	O11826_9HIV1	O11826 human immun

432	23	24.5	21	2	O11827_9HIV1	O11827 human immun
433	23	24.5	21	2	O11831_9HIV1	O11831 human immun
434	23	24.5	21	2	O11838_9HIV1	O11838 human immun
435	23	24.5	22	1	UVSX_BPT2	Q06727 bacteriopha
436	23	24.5	22	2	Q9UEY3_HUMAN	Q9uey3 homo sapien
437	23	24.5	22	2	Q4XUD0_PLACH	Q4xud0 plasmodium
438	23	24.5	23	2	Q4XTG0_PLACH	Q4xtg0 plasmodium
439	23	24.5	23	2	Q4Z0X5_PLABE	Q4z0x5 plasmodium
440	23	24.5	23	2	Q9XZW1_9CAEN	Q9xzw1 littorina a
441	23	24.5	23	2	Q9XZW4_LITLI	Q9xzw4 littorina l
442	23	24.5	23	2	Q9XZZ7_9CAEN	Q9xzz7 littorina s
443	23	24.5	23	2	Q9Y003_9CAEN	Q9y003 melarhaphe
444	23	24.5	23	2	Q68983_9ALPH	Q68983 suid herpes
445	23	24.5	23	2	Q98YK6_9HIV1	Q98yk6 human immun
446	23	24.5	24	2	Q4XJG7_PLACH	Q4xjg7 plasmodium
447	23	24.5	24	2	Q4XV06_PLACH	Q4xv06 plasmodium
448	23	24.5	24	2	Q4YMW5_PLABE	Q4ymw5 plasmodium
449	23	24.5	24	2	Q4Z471_PLABE	Q4z471 plasmodium
450	23	24.5	24	2	Q29403_SHEEP	Q29403 ovis aries
451	23	24.5	24	2	Q6ZZ53_9CARY	Q6zz53 silene coel
452	23	24.5	24	2	Q9K8M1_BACHD	Q9k8m1 bacillus ha
453	23	24.5	25	2	Q4YA76_PLABE	Q4ya76 plasmodium
454	23	24.5	25	2	Q4YTS4_PLABE	Q4yts4 plasmodium
455	23	24.5	25	2	O77602_PAPAN	O77602 papio anubi
456	23	24.5	25	2	O77603_THEGE	O77603 theropithec
457	23	24.5	25	2	O77604_MACMU	O77604 macaca mula
458	23	24.5	25	2	O77605_MANLE	O77605 mandrillus
459	23	24.5	25	2	O77606_MANSP	O77606 mandrillus
460	23	24.5	25	2	O77607_LOPAT	O77607 lophocebus
461	23	24.5	25	2	O77827_LOPAA	O77827 lophocebus
462	23	24.5	25	2	O77828_CERTO	O77828 cercocebus
463	23	24.5	25	2	O77829_CERGC	O77829 cercocebus
464	23	24.5	25	2	O77831_CERMI	O77831 cercopithec
465	23	24.5	25	2	O77832_CERAE	O77832 cercopithec
466	23	24.5	25	2	Q7M156_BACTU	Q7m156 bacillus th
467	23	24.5	25	2	Q53I74_RAT	Q53i74 rattus norv
468	23	24.5	25	2	Q6SWG7_HCMV	Q6swg7 human cytom
469	23	24.5	25	2	Q56CD0_9HIV1	Q56cd0 human immun
470	23	24.5	25	2	Q56CF6_9HIV1	Q56cf6 human immun
471	23	24.5	25	2	Q56CF7_9HIV1	Q56cf7 human immun
472	23	24.5	25	2	Q9DU23_9HIV1	Q9du23 human immun
473	23	24.5	26	1	RL16_BACST	P23310 bacillus st
474	23	24.5	26	2	Q5ZQW9_9CAUD	Q5zqw9 bacteriopha
475	23	24.5	26	2	Q9QV79_9MURI	Q9qv79 rattus sp.
476	23	24.5	26	2	Q85461_9RETR	Q85461 avian myelo
477	23	24.5	27	2	Q7Z2G0_HUMAN	Q7z2g0 homo sapien
478	23	24.5	27	2	Q4Y431_PLACH	Q4y431 plasmodium
479	23	24.5	27	2	Q4YFL7_PLABE	Q4yfl7 plasmodium
480	23	24.5	27	2	Q4YZ78_PLABE	Q4yz78 plasmodium
481	23	24.5	27	2	Q9TM43_CYACA	Q9tm43 cyanidium c
482	23	24.5	28	2	Q7SAK0_NEUCR	Q7sak0 neurospora
483	23	24.5	28	2	Q4YFV6_PLABE	Q4yfv6 plasmodium
484	23	24.5	28	2	Q45QJ8_RAT	Q45qj8 rattus norv
485	23	24.5	29	2	O35358_RAT	O35358 rattus norv
486	23	24.5	29	2	P97599_RAT	P97599 rattus norv
487	23	24.5	29	2	Q9WVC4_MOUSE	Q9wvc4 mus musculu
488	23	24.5	29	2	Q90817_CHICK	Q90817 gallus gall
489	23	24.5	30	2	Q4XZM1_PLACH	Q4xzm1 plasmodium
490	23	24.5	30	2	Q4YDJ7_PLABE	Q4ydj7 plasmodium
491	23	24.5	30	2	Q7RHK1_PLAYO	Q7rhk1 plasmodium
492	23	24.5	30	2	Q7RHQ9_PLAYO	Q7rhq9 plasmodium

493	23	24.5	30	2	Q03618_STRHY	Q03618 streptomyce
494	23	24.5	30	2	Q47Z49_COLP3	Q47z49 colwellia p
495	23	24.5	30	2	Q4MGH8_BACCE	Q4mgh8 bacillus ce
496	23	24.5	30	2	Q9R5A3_9PSED	Q9r5a3 pseudomonas
497	23	24.5	30	2	Q57BN2_BRUAB	Q57bn2 brucella ab
498	23	24.5	30	2	Q72B97_DESVH	Q72b97 desulfovibr
499	23	24.5	30	2	Q7VKB9_HAEDU	Q7vkb9 haemophilus
500	23	24.5	30	2	Q8FZ53_BRUSU	Q8fz53 brucella su
501	23	24.5	30	2	Q2YRK9_BRUA2	Q2yrk9 brucella ab
502	23	24.5	30	2	Q4T6V6_TETNG	Q4t6v6 tetraodon n
503	23	24.5	30	2	Q9W7N3_MORSA	Q9w7n3 morone saxa
504	22.5	23.9	23	2	Q4XJB4_PLACH	Q4xjb4 plasmodium
505	22.5	23.9	25	2	Q4RAH1_TETNG	Q4rah1 tetraodon n
506	22.5	23.9	26	2	Q4YXA8_PLABE	Q4yxa8 plasmodium
507	22.5	23.9	30	2	Q9TWM4_MANSE	Q9twm4 manduca sex
508	22.5	23.9	30	2	Q8SMQ5_9AQUA	Q8smq5 ilex repand
509	22	23.4	9	2	Q67AQ7_HUMAN	Q67aq7 homo sapien
510	22	23.4	9	2	Q7EXP6_HORVD	Q7exp6 hordeum vul
511	22	23.4	9	2	Q9FEC0_HORVU	Q9fec0 hordeum vul
512	22	23.4	10	2	Q8GZC8_HORVU	Q8gzc8 hordeum vul
513	22	23.4	13	1	SODM_ARTDA	P83289 arthrobotry
514	22	23.4	14	1	PLYB1_POLPI	P84388 polybia pau
515	22	23.4	14	2	Q7M0Q6_9THEM	Q7m0q6 thermotoga
516	22	23.4	15	2	Q56IZ1_9FLAV	Q56iz1 tick-borne
517	22	23.4	15	2	Q5R3U5_XENLA	Q5r3u5 xenopus lae
518	22	23.4	16	2	Q6JQ71_HBV	Q6jq71 hepatitis b
519	22	23.4	17	1	PATS_ANASP	O52748 anabaena sp
520	22	23.4	17	2	Q7RQU2_PLAYO	Q7rqu2 plasmodium
521	22	23.4	17	2	Q3V3P2_MOUSE	Q3v3p2 mus musculu
522	22	23.4	17	2	Q811C1_MOUSE	Q811c1 mus musculu
523	22	23.4	17	2	Q5R3U2_XENLA	Q5r3u2 xenopus lae
524	22	23.4	17	2	Q7T080_9AVES	Q7t080 anser anser
525	22	23.4	17	2	Q7T081_ANAPL	Q7t081 anas platyr
526	22	23.4	18	2	Q8RU82_MAIZE	Q8ru82 zea mays (m
527	22	23.4	19	2	Q4Z5V1_PLABE	Q4z5v1 plasmodium
528	22	23.4	19	2	Q9BGH0_PIG	Q9bgh0 sus scrofa
529	22	23.4	19	2	Q38371_BPMS2	Q38371 bacteriopha
530	22	23.4	20	1	GUAA_LACSN	P83540 lactobacill
531	22	23.4	20	2	Q9TWN5_THESE	Q9twn5 theileria s
532	22	23.4	20	2	Q9S8K2_SOLTU	Q9s8k2 solanum tub
533	22	23.4	20	2	Q7M195_THEAQ	Q7m195 thermus aqu
534	22	23.4	20	2	Q9QUZ1_9MURI	Q9quz1 rattus sp.
535	22	23.4	21	1	OMP44_PASHA	P80228 pasteurella
536	22	23.4	21	1	THAN_PODMA	P55788 podisus mac
537	22	23.4	21	2	Q4XNE6_PLACH	Q4xne6 plasmodium
538	22	23.4	21	2	Q4XX24_PLACH	Q4xx24 plasmodium
539	22	23.4	21	2	Q4Y631_PLACH	Q4y631 plasmodium
540	22	23.4	21	2	Q4Y8P3_PLACH	Q4y8p3 plasmodium
541	22	23.4	21	2	Q4Y9Z3_PLABE	Q4y9z3 plasmodium
542	22	23.4	21	2	Q9ZYB7_9HYME	Q9zyb7 spinaria sp
543	22	23.4	21	2	Q93CI4_ECOLI	Q93ci4 escherichia
544	22	23.4	22	2	Q4XAK9_PLACH	Q4xak9 plasmodium
545	22	23.4	22	2	Q9IAV6_9PASS	Q9iav6 acanthiza n
546	22	23.4	22	2	Q9IAV7_9PASS	Q9iav7 acanthiza l
547	22	23.4	22	2	Q9IAV8_9PASS	Q9iav8 acanthiza r
548	22	23.4	22	2	Q9IAV9_9PASS	Q9iav9 acanthiza u
549	22	23.4	22	2	Q9IAW0_9PASS	Q9iaw0 acanthiza r
550	22	23.4	22	2	Q9IAW1_9PASS	Q9iaw1 acanthiza i
551	22	23.4	22	2	Q9IAW2_9PASS	Q9iaw2 acanthiza i
552	22	23.4	22	2	Q9IAW3_9PASS	Q9iaw3 acanthiza p
553	22	23.4	22	2	Q9IAW4_ACAKA	Q9iaw4 acanthiza k

554	22	23.4	22	2	Q9IAW5_9PASS	Q9iaw5 acanthiza e
555	22	23.4	22	2	Q9IAW6_9PASS	Q9iaw6 acanthiza c
556	22	23.4	22	2	Q9IAW7_9PASS	Q9iaw7 acanthiza a
557	22	23.4	22	2	Q9IAW8_9PASS	Q9iaw8 smicrornis
558	22	23.4	22	2	Q9IAW9_9PASS	Q9iaw9 gerygone fu
559	22	23.4	22	2	Q9IAX0_9PASS	Q9iax0 aphelocepha
560	22	23.4	22	2	Q9IAX1_9PASS	Q9iax1 sericornis
561	22	23.4	22	2	Q8AEW5_9HIV1	Q8aew5 human immun
562	22	23.4	22	2	Q8AEW9_9HIV1	Q8aew9 human immun
563	22	23.4	23	2	Q4XXR5_PLACH	Q4xxr5 plasmodium
564	22	23.4	23	2	Q4YRL7_PLABE	Q4yrl7 plasmodium
565	22	23.4	23	2	Q7RSU3_PLAYO	Q7rsu3 plasmodium
566	22	23.4	23	2	O18841_PIG	O18841 sus scrofa
567	22	23.4	23	2	Q4JQP8_PIG	Q4jqp8 sus scrofa
568	22	23.4	23	2	Q9T354_MACSY	Q9t354 macaca sylv
569	22	23.4	23	2	Q3KU33_STRCR	Q3ku33 streptococc
570	22	23.4	23	2	Q47WG5_COLP3	Q47wg5 colwellia p
571	22	23.4	23	2	Q57162_ENTFA	Q57162 enterococcu
572	22	23.4	23	2	Q5PFC9_SALPA	Q5pfc9 salmonella
573	22	23.4	23	2	Q8E018_STRA5	Q8e018 streptococc
574	22	23.4	23	2	Q8Z974_SALTI	Q8z974 salmonella
575	22	23.4	24	2	Q4XYM2_PLACH	Q4xym2 plasmodium
576	22	23.4	24	2	Q4YB25_PLABE	Q4yb25 plasmodium
577	22	23.4	24	2	Q4Z5N0_PLABE	Q4z5n0 plasmodium
578	22	23.4	24	2	Q94370_CAEEL	Q94370 caenorhabdi
579	22	23.4	24	2	Q9TRE8_BOVIN	Q9tre8 bos taurus
580	22	23.4	25	1	CPI2_SOLTU	P24744 solanum tub
581	22	23.4	25	1	HCY3_MAISQ	P82304 maia squina
582	22	23.4	25	1	RL29_BREVE	Q9r4p0 brevundimon
583	22	23.4	25	1	TFDC2_COMAC	P83116 comamonas a
584	22	23.4	25	2	Q4X3H5_PLACH	Q4x3h5 plasmodium
585	22	23.4	25	2	Q4XCD1_PLACH	Q4xcd1 plasmodium
586	22	23.4	25	2	Q4Y5T2_PLACH	Q4y5t2 plasmodium
587	22	23.4	25	2	Q4Y9R3_PLABE	Q4y9r3 plasmodium
588	22	23.4	25	2	Q7R8K6_PLAYO	Q7r8k6 plasmodium
589	22	23.4	25	2	Q7RAC5_PLAYO	Q7rac5 plasmodium
590	22	23.4	25	2	Q7RJP0_PLAYO	Q7rjp0 plasmodium
591	22	23.4	25	2	Q9BM55_9BIVA	Q9bm55 chione canc
592	22	23.4	25	2	Q6JDJ8_CANFA	Q6jdj8 canis famil
593	22	23.4	25	2	Q40972_PINRA	Q40972 pinus radia
594	22	23.4	25	2	Q40973_PINRA	Q40973 pinus radia
595	22	23.4	25	2	Q56C54_9HIV1	Q56c54 human immun
596	22	23.4	25	2	Q56C55_9HIV1	Q56c55 human immun
597	22	23.4	25	2	Q56C56_9HIV1	Q56c56 human immun
598	22	23.4	25	2	Q56C57_9HIV1	Q56c57 human immun
599	22	23.4	25	2	Q56C58_9HIV1	Q56c58 human immun
600	22	23.4	25	2	Q56C59_9HIV1	Q56c59 human immun
601	22	23.4	25	2	Q56C60_9HIV1	Q56c60 human immun
602	22	23.4	25	2	Q56C61_9HIV1	Q56c61 human immun
603	22	23.4	25	2	Q56C62_9HIV1	Q56c62 human immun
604	22	23.4	25	2	Q56C63_9HIV1	Q56c63 human immun
605	22	23.4	25	2	Q56C65_9HIV1	Q56c65 human immun
606	22	23.4	25	2	Q56C66_9HIV1	Q56c66 human immun
607	22	23.4	25	2	Q56C67_9HIV1	Q56c67 human immun
608	22	23.4	25	2	Q56C69_9HIV1	Q56c69 human immun
609	22	23.4	25	2	Q56C70_9HIV1	Q56c70 human immun
610	22	23.4	25	2	Q56C71_9HIV1	Q56c71 human immun
611	22	23.4	25	2	Q56C72_9HIV1	Q56c72 human immun
612	22	23.4	25	2	Q56C73_9HIV1	Q56c73 human immun
613	22	23.4	25	2	Q56C74_9HIV1	Q56c74 human immun
614	22	23.4	25	2	Q56C75_9HIV1	Q56c75 human immun

10/715,810

RESULT 3
ADZ69738
ID ADZ69738 standard; peptide; 20 AA.
XX
AC ADZ69738;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:13.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Example 1; SEQ ID NO 13; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 20 AA;

aa 785-803

Query Match 89.2%; Score 91; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 7e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

RESULT 4
ADZ69808
ID ADZ69808 standard; peptide; 20 AA.
XX
AC ADZ69808;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:83.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 83; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 20 AA;

  Query Match   89.2%; Score 91; DB 9; Length 20;
  Best Local Similarity   100.0%; Pred. No. 7e-08;
  Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

qa 785-803

```
Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

RESULT 5
ADZ69753
ID ADZ69753 standard; peptide; 20 AA.
XX
AC ADZ69753;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:28.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Example 1; SEQ ID NO 28; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 20 AA;

  Query Match   89.2%; Score 91; DB 9; Length 20;
  Best Local Similarity   100.0%; Pred. No. 7e-08;
  Matches   17; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

ca 785-803

```
Qy          3 FLNQCSVSYLMNSMIPY 19
              |||||||||||||||||
Db          1 FLNQCSVSYLMNSMIPY 17
```

ADJ82841
ID ADJ82841 standard; peptide; 14 AA.
XX
AC ADJ82841;
XX
DT 06-MAY-2004 (first entry)
XX
DE Tetanus Tet(639)V epitope for fusion peptide vaccine.
XX
KW immunostimulant; vaccine; cytomegalovirus; fusion peptide;
KW T helper epitope; CTL epitope; PADRE; tetanus epitope; DNA adjuvant;
KW immune system.
XX
OS Clostridium tetani.
OS Unidentified.
XX
PN WO2004000873-A2.
XX
PD 31-DEC-2003.
XX
PF 25-JUN-2003; 2003WO-US019848.
XX
PR 25-JUN-2002; 2002US-0391088P.
XX
PA (CITY) CITY OF HOPE.
XX
PI Diamond DJ;
XX
DR WPI; 2004-082471/08.
XX
PT New cytomegalovirus (CMV) vaccine comprising a fusion peptide composed of
PT a T helper epitope fused to a CMV CTL epitope peptide, useful in
PT manufacturing a medicament for modifying the immune system of a mammal
PT against CMV.
XX
PS Disclosure; SEQ ID NO 4; 52pp; English.
XX
CC The invention relates to a cytomegalovirus vaccine comprising a fusion
CC peptide composed of a T helper epitope fused to a CMV CTL epitope
CC peptide. The T helper epitope is PADRE or a tetanus epitope selected from
CC tetanus heavy chain (590-603), tetanus heavy chain (615-629), tetanus
CC heavy chain (639-652), tetanus heavy chain (830-843), and tetanus heavy
CC chain (947-967). The CMV pp65 CTL epitope peptide is selected from
CC pp65(13-24), pp65(186-196), pp65(188-195), pp65(265-275), pp65(363-373),
CC pp65(369-379), pp65(367-379), pp65(495-503), and pp65(417-426),
CC preferably pp65(495-503). The vaccine may further comprise a DNA
CC adjuvant. The vaccine is useful in the manufacture of a medicament for
CC modifying the immune system of a mammal against CMV. This sequence
CC corresponds to the tetanus epitope Tet(639)V used in the vaccine of the
CC invention.
XX
SQ Sequence 14 AA;

Query Match 56.6%; Score 56; DB 8; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.048;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 IIPYIGPALNI 13
              |:||||||||||
Db          4 IVPYIGPALNI 14
```

ADJ82841
ID ADJ82841 standard; peptide; 14 AA.
XX
AC ADJ82841;
XX
DT 06-MAY-2004 (first entry)
XX
DE Tetanus Tet(639)V epitope for fusion peptide vaccine.
XX
KW immunostimulant; vaccine; cytomegalovirus; fusion peptide;
KW T helper epitope; CTL epitope; PADRE; tetanus epitope; DNA adjuvant;
KW immune system.
XX
OS Clostridium tetani.
OS Unidentified.
XX
PN WO2004000873-A2.
XX
PD 31-DEC-2003.
XX
PF 25-JUN-2003; 2003WO-US019848.
XX
PR 25-JUN-2002; 2002US-0391088P.
XX
PA (CITY) CITY OF HOPE.
XX
PI Diamond DJ;
XX
DR WPI; 2004-082471/08.
XX
PT New cytomegalovirus (CMV) vaccine comprising a fusion peptide composed of
PT a T helper epitope fused to a CMV CTL epitope peptide, useful in
PT manufacturing a medicament for modifying the immune system of a mammal
PT against CMV.
XX
PS Disclosure; SEQ ID NO 4; 52pp; English.
XX
CC The invention relates to a cytomegalovirus vaccine comprising a fusion
CC peptide composed of a T helper epitope fused to a CMV CTL epitope
CC peptide. The T helper epitope is PADRE or a tetanus epitope selected from
CC tetanus heavy chain (590-603), tetanus heavy chain (615-629), tetanus
CC heavy chain (639-652), tetanus heavy chain (830-843), and tetanus heavy
CC chain (947-967). The CMV pp65 CTL epitope peptide is selected from
CC pp65(13-24), pp65(186-196), pp65(188-195), pp65(265-275), pp65(363-373),
CC pp65(369-379), pp65(367-379), pp65(495-503), and pp65(417-426),
CC preferably pp65(495-503). The vaccine may further comprise a DNA
CC adjuvant. The vaccine is useful in the manufacture of a medicament for
CC modifying the immune system of a mammal against CMV. This sequence
CC corresponds to the tetanus epitope Tet(639)V used in the vaccine of the
CC invention.
XX
SQ Sequence 14 AA;

Query Match 56.6%; Score 56; DB 8; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.048;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IIPYIGPALNI 13
:|||||||||
Db 4 IVPYIGPALNI 14

RESULT 5
ADZ69794
ID ADZ69794 standard; peptide; 8 AA.
XX
AC ADZ69794;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:69.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 69; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 8 AA;

Query Match 44.8%; Score 47; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

547-565

```
Qy          2 YTMFHYLR 9
              ||||||||
Db          1 YTMFHYLR 8
```

1

ADZ69798
ID ADZ69798 standard; peptide; 30 AA.
XX
AC ADZ69798;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:73.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 73; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 30 AA;

Query Match 58.0%; Score 58; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ATEAAMFLGWV 19

qa589-607

```
                ||||||||||
Db          1 ATEAAMFLGWV 11
```

```
 Sequence 74, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 627-649)
US-10-715-810-74

  Query Match             100.0%;  Score 99;  DB 5;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-09;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TIIIPYIGPALNIGNMLYK 19
              ||||||||||||||||||
Db          5 TIIIPYIGPALNIGNMLYK 23
```

RESULT 4
ADZ69803
ID ADZ69803 standard; peptide; 9 AA.
XX
AC ADZ69803;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:78.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 78; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 9 AA;

Query Match 43.9%; Score 43; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 VNTQIDLIR 15
              |||||||||
Db          1 VNTQIDLIR 9
```

RESULT 20
ADZ69802
ID ADZ69802 standard; peptide; 9 AA.
XX
AC ADZ69802;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:77.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 77; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 9 AA;

  Query Match   35.7%; Score 35; DB 9; Length 9;
  Best Local Similarity   100.0%; Pred. No. 2.1e+06;
  Matches   6; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

715-733

```
Qy          1 TNWLAK 6
              ||||||
Db          4 TNWLAK 9
```

RESULT 3
ADZ69805
ID ADZ69805 standard; peptide; 15 AA.
XX
AC ADZ69805;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:80.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 80; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 15 AA;

  Query Match   78.4%; Score 80; DB 9; Length 15;
  Best Local Similarity   100.0%; Pred. No. 3.2e-05;
  Matches   15; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          3 AIINYQYNQYTEEEK 17
              ||||||||||||||||
Db          1 AIINYQYNQYTEEEK 15
```

RESULT 2
ADZ69820
ID ADZ69820 standard; peptide; 19 AA.
XX
AC ADZ69820;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:95.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 95; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 19 AA;

ga 981-999

Query Match 75.5%; Score 74; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GEIIWTLQDTQEIK 14
              ||||||||||||||
Db          6 GEIIWTLQDTQEIK 19
```

```
RESULT 41
US-10-715-810-99
; Sequence 99, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 1035-1056)
US-10-715-810-99

  Query Match             28.6%;  Score 32;  DB 5;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 7.2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NNIMFK 6
              ||||||
Db         17 NNIMFK 22
```

aa 1051-1069

RESULT 2
ADZ69830
ID ADZ69830 standard; peptide; 20 AA.
XX
AC ADZ69830;
XX
DT 28-JUL-2005 (first entry)
XX
DE Botulinum toxin type A peptide SEQ ID NO:105.
XX
KW toxin; muscular-gen.; analgesic; antimigraine; cns-gen.;
KW autonomic nervous system disease; pain; neuromuscular disease;
KW cervical dystonia; migraine.
XX
OS Clostridium botulinum.
XX
PN US2005106182-A1.
XX
PD 19-MAY-2005.
XX
PF 17-NOV-2003; 2003US-00715810.
XX
PR 17-NOV-2003; 2003US-00715810.
XX
PA (LISS/) LI S.
PA (AOKI/) AOKI K R.
XX
PI Li S, Aoki KR;
XX
DR WPI; 2005-365766/37.
XX
PT Treating botulinum toxin intoxication in a mammal, comprises
PT administering a rescue agent comprising an inactive botulinum toxin and a
PT modified nontoxic nonhemagglutinin to a mammal.
XX
PS Disclosure; SEQ ID NO 105; 61pp; English.
XX
CC The invention relates to a method (M1) for treating botulinum toxin
CC intoxication in a mammal. (M1) comprises administering at least one
CC rescue agent (I) to a mammal. Also described: (1) a botulinum toxin (II)
CC being glycosylated, having reduced antigenicity, and being inactive; (2)
CC making (M2) a di-chain botulinum in a non-Clostridium botulinum cell or
CC in a cell free system; (3) a modified nontoxic nonhemagglutinin
CC comprising a nontoxic nonhemagglutinin and a targeting group; and (4) a
CC non-Clostridium botulinum cell (III) comprising a vector operatively
CC harboring a nucleotide sequence encoding a single chain botulinum toxin
CC and a vector operatively harboring nucleotide sequence encoding a
CC nontoxic nonhemagglutinin. (II) is useful for treating a muscular
CC condition, an autonomic nervous system disorder and/or pain, which
CC involves administering (II) to the mammal in need of the toxins. (II) is
CC also useful for the treatment of neuromuscular disorders, cervical
CC dystonia and migraine. The present sequence represents a Clostridium
CC botulinum toxin type A peptide sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 20 AA;

aa 275-1296

Query Match 93.1%; Score 121; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 TLGCSWEFIPVDDGWGERPL 22
              ||||||||||||||||||||
Db          1 TLGCSWEFIPVDDGWGERPL 20
```

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 13:45:45 ; Search time 57.1624 Seconds
(without alignments)
153.966 Million cell updates/sec

Title: US-10-821-669-1_COPY_673_691
Perfect score: 91
Sequence: 1 IPVLGTFALVSYIANKVLT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 526792

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	37.4	28	4	[redacted]	Sequence 28518, A

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:30:50 ; Search time 99.3 Seconds
(without alignments)
176.992 Million cell updates/sec

Title: US-10-821-669-1_COPY_589_607
Perfect score: 100
Sequence: 1 DYVKKVNKATEAAMFLGWV 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 37017

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33	33.0	20	2	Q9ZY85_BOMTE	Q9zy85 bombus terr
2	33	33.0	30	2	Q73RF8_TREDE	Q73rf8 treponema d

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_491_509
Perfect score: 99
Sequence: 1 EENISLDLIQQYYLTFNFD 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	99	100.0	19	9	ADW11044	Adw11044 Clostridi
2	99	100.0	27	9	ADW11103	Adw11103 Clostridi
3	37	37.4	14	9	ADV55232	Adv55232 G protein

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 107.179 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_1275_1296
Perfect score: 130
Sequence: 1 SRTLGCSWEFIPVDDGWGERPL 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	130	100.0	22	9	ADW11100	Adw11100 Clostridi
2	121	93.1	20	9	ADZ69830	Adz69830 Botulinum
3	70	53.8	20	2	AAR47809	Aar47809 Sequence
4	70	53.8	21	2	AAR04088	Aar04088 The carbo
5	70	53.8	21	2	AAR47810	Aar47810 Sequence
6	45	34.6	19	5	AAU85629	Aau85629 Lung tumo

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_1121_1139
Perfect score: 104
Sequence: 1 KYVDVNNVGIRGYMYLKGP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	104	100.0	19	9	ADW11089	Adw11089 Clostridi

```
AAW11973
ID   AAW11973 standard; peptide; 8 AA.
XX
AC   AAW11973;
XX
DT   02-APR-1997  (first entry)
XX
DE   T-cell epitope #4 from tetanus toxoid.
XX
KW   T-cell epitope; antigen; T-cell determinant; receptor; MHC protein; bird;
KW   HIV sf2; herpes simplex virus; antigen gD2; tetanus toxoid; vaccine; HSV;
KW   mammal; gp120; immune response; B-cell antigen.
XX
OS   Synthetic.
XX
PN   WO9518148-A1.
XX
PD   06-JUL-1995.
XX
PF   28-DEC-1993;   93WO-US011703.
XX
PR   28-DEC-1993;   93WO-US011703.
XX
PA   (CHIR-) CHIRON MIMOTOPES PTY LTD.
XX
PI   Geysen HM,  Rodda SJ;
XX
DR   WPI; 1995-246333/32.
XX
PT   T cell epitope peptide(s) - useful for detecting exposure of a subject to
PT   an antigen or pathogen, and in vaccines for birds and mammals.
XX
PS   Claim 1; Page 45; 57pp; English.
XX
CC   AAW11953-W11976 represent T-cell epitope peptides. T-cell epitopes (also
CC   known as T-cell determinants) are peptides (or regions of a protein)
CC   which bind to T-cell antigen receptors in conjugation with MHC proteins.
CC   These sequences were the most antigenic peptides obtained from pools of
CC   peptides created from the HIV sf2 gp120 (AAW11953-W11960), herpes simplex
CC   virus antigen gD2 (AAW11961-W11969), and tetanus toxoid (AAW11970-
CC   W11976). These sequences can be used in methods for detecting exposure of
CC   a mammal or bird to an antigen, and for increasing the number of T-cells
CC   specific for an antigen. The peptides can also be used in a method for
CC   determining T-cell epitopes specific for an antigen. These methods allow
CC   for the identification of T-cell determinants. The T-cell epitope
CC   peptides can be used in a vaccine for inducing an immune response in a
CC   bird or mammal. The vaccine also contains a B-cell antigen, preferably
CC   herpes simplex virus gD2 or HIV sf2 gp120 (see AAW11977), and a carrier
XX
SQ   Sequence 8 AA;

  Query Match             42.4%;  Score 42;  DB 2;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 2.1e+06;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPA 10
              |:||||||
Db          1 IVPYIGPA 8
```

631-649

ID AAW05608 standard; peptide; 16 AA.
XX
AC AAW05608;
XX
DT 10-DEC-1996 (first entry)
XX
DE Tetanus toxin helper T cell epitope #5.
XX
KW Immunoglobulin; IgE; membrane protein; human; epsilon chain; hepatitis B;
KW membrane anchoring domain; helper T cell; surface antigen; core antigen;
KW pertussis toxin; tetanus toxin; measles virus F protein; immunotherapy;
KW Chlamydia trachomatis major outer membrane protein; immunogen; vaccine;
KW diphtheria toxin; plasmodium falciparum; circumsporozoite; E. coli TraT;
KW schistosoma mansoni; triose phosphate isomerase; allergenic reaction;
KW allergic rhinitis; food allergy; anaphylaxis; virally-induced asthma;
KW antihistamine; decongestant; beta-2 agonist; immunosuppression;
KW corticosteroid.
XX
OS Synthetic.
XX
PN WO9612740-A1.
XX
PD 02-MAY-1996.
XX
PF 25-OCT-1995; 95WO-US013841.
XX
PR 25-OCT-1994; 94US-00328519.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY, Walfield AM;
XX
DR WPI; 1996-230555/23.
XX
PT Peptide immunogen useful in treatment of allergy - comprises membrane-
PT bound IgE epsilon-chain peptide synthesised linearly in tandem with T
PT helper epitope peptide.
XX
PS Claim 2; Page 19; 53pp; English.
XX
CC AAW05957-W05616 represent helper T cell epitopes used in the peptide
CC immunogens of the invention. This sequence represents the tetanus toxin
CC helper T cell antigen. The peptides of the invention contain one of these
CC sequences, and a membrane-bound immunoglobulin E (IgE) fragment (see
CC AAW05595 and AAW05596). The peptide immunogens of the invention can be
CC used in vaccines for the immunotherapeutic treatment of allergenic
CC reactions, including allergic rhinitis, food allergies, anaphylaxis, or
CC virally-induced asthma. The immunogens overcome the short effective
CC period of antihistamines, decongestants, and beta-2 agonists, while
CC preventing the broad immunosuppression of corticosteroids. The peptides
CC do not have the potential side effects of restlessness or sedation
CC (associated with antihistamines), associated increased morbidity in
CC asthmatics (as seen with beta-2 agonists) and adverse hormonal activities
CC (observed in corticosteroid users)
XX
SQ Sequence 16 AA;

631-649

Query Match 56.6%; Score 56; DB 2; Length 16;
Best Local Similarity 90.9%; Pred. No. 0.055;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 IIPYIGPALNI 13
              |:|||||||||
Db          5 IVPYIGPALNI 15
```

```
AAY96457
ID   AAY96457 standard; peptide; 20 AA.
XX
AC   AAY96457;
XX
DT   12-SEP-2000  (first entry)
XX
DE   Tetanus toxin (TTD)-specific peptide residues 632-651.
XX
KW   Tetanus toxin; DTX; universal epitope; CD4-positive; immunodominant;
KW   antigen; infection; vaccine; immunostimulatory.
XX
OS   Synthetic.
XX
PN   WO200032626-A1.
XX
PD   08-JUN-2000.
XX
PF   24-NOV-1999;   99WO-US028039.
XX
PR   25-NOV-1998;   98US-00199748.
XX
PA   (MINU ) UNIV MINNESOTA.
PA   (CONT/) CONTI-FINE B M.
XX
PI   Conti-Fine BM;
XX
DR   WPI; 2000-412286/35.
XX
PT   Isolated and purified peptide for immunization of mammal against
PT   infectious agent comprises amino acid sequence similar or identical to
PT   portion of amino acid sequence of antigen from infectious agent.
XX
PS   Example 4; Page 66; 108pp; English.
XX
CC   Peptides AAY96457-56 are tetanus toxoid (TTD) specific peptides capable
CC   of acting as universal epitopes. The peptides seem to be recognized by
CC   CD4 positive cells in humans, irrespective of their human leukocyte
CC   antigen (HLA) class II haplotype. These peptides and diphtheria toxin
CC   specific peptides (e.g. AAY96450-55) are useful as universal epitopes. A
CC   common structural feature of the peptides that may give them an advantage
CC   during processing is that they all include, or are flanked by, both at
CC   the N- and C-terminal ends, sequence regions forming relatively
CC   unstructured loops fully exposed to the solvent. Flanking exposed loops
CC   may be important for IRS formation as the loops would make easy targets
CC   for processing enzymes, resulting in the fast release of sequence
CC   segments embedded in the hydrophobic core of the antigenic molecule. The
CC   universal peptide epitopes can be used in vaccines against infectious
CC   agents (e.g. viruses, bacteria and fungi). The invention also provides
CC   methods of identifying immunogenic epitopes and IRS
XX
SQ   Sequence 20 AA;

  Query Match             56.6%;  Score 56;  DB 3;  Length 20;
  Best Local Similarity   90.9%;  Pred. No. 0.071;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:||||||||||
Db         10 IVPYIGPALNI 20
```

```
AAR82582
ID   AAR82582 standard; peptide; 16 AA.
XX
AC   AAR82582;
XX
DT   13-JUN-1996  (first entry)
XX
DE   Tetanus toxin helper T cell epitope, TT5.
XX
KW   IgE; CH4; immunoglobulin; epsilon; immunogen; helper T cell; epitope;
KW   vaccine; allergy; antibody; constant heavy chain.
XX
OS   Clostridium tetani.
XX
PN   WO9526365-A1.
XX
PD   05-OCT-1995.
XX
PF   24-MAR-1995;   95WO-US003741.
XX
PR   28-MAR-1994;   94US-00218461.
PR   25-OCT-1994;   94US-00328912.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 1995-351297/45.
XX
PT   Synthetic peptide-based immunogen contg. IgE CH4 peptide and helper T
PT   cell epitope - useful for eliciting antibody prodn. for allergy
PT   treatment.
XX
PS   Claim 3; Page 23; 87pp; English.
XX
CC   AAR82571-91 are helper T cell epitopes which can be used in the
CC   preparation of a peptide immunogen that is useful in vaccines for
CC   treating allergic reactions. In the immunogen an IgE CH4 peptide is
CC   attached C-terminally to a series of amino acids including a helper T
CC   cell epitope. The immunogen may also opt. contain a fatty acid or fatty
CC   acid derivative, an invasin domain or alpha-NH2. The immunogen produces
CC   high titres of antibodies to the effector site in human IgE heavy chain
CC   (the CH4 domain peptide) which inhibit mast cell activation and reduce
CC   allergen-induced IgE prodn. The immunogens may be used in either a
CC   radially branching multimeric form or a linearly arranged monomeric form
XX
SQ   Sequence 16 AA;

  Query Match             52.5%;  Score 52;  DB 2;  Length 16;
  Best Local Similarity   90.0%;  Pred. No. 0.25;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALN 12
              |:|||||||
Db          5 IVPYIGPALN 14
```

AAR86583
ID AAR86583 standard; protein; 7 AA.
XX
AC AAR86583;
XX
DT 28-JUN-1996 (first entry)
XX
DE Autotaxin peptide fragment ATX-209.
XX
KW Autotaxin; ATX; cytokine; autocrine motility stimulating protein; AMF;
KW melanoma cell; tumour; antibody; cancer diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO9532221-A2.
XX
PD 30-NOV-1995.
XX
PF 24-MAY-1995; 95WO-US006613.
XX
PR 25-MAY-1994; 94US-00249182.
PR 28-NOV-1994; 94US-00346455.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Stracke M, Liotta L, Schiffmann E, Krutzch J, Murata J;
XX
DR WPI; 1996-020533/02.
XX
PT Autotaxin motility stimulating protein, and DNA encoding it - used in
PT cancer diagnosis and therapy.
XX
PS Claim 4; Page 12; 112pp; English.
XX
CC AAR86559-R86596 represent autotaxin (ATX) and fragments of it. ATX is an
CC autocrine motility stimulating protein which is present in cancer cells.
CC ATX stimulates both random and directed migration of melanoma cells. The
CC tumourous form of ATX is a secreted protein, while the transmembrane
CC bound form is not present in tumour cells. The cDNA encoding this
CC sequence can be used in a vector, to transform cells. The recombinant
CC cells can then be used to produce the peptide sequences. Antibodies
CC specific for these sequences can be produced, and can be used in cancer
CC diagnosis and therapy. Different sites of localisation of the protein are
CC utilised for diagnosis and prognosis of the stages of tumour progression.
CC The sequences can be used in treatment methods to advantageously block
CC the activity of the secreted form of AXT, while having little effect on
CC the membrane form of AXT
XX
SQ Sequence 7 AA;

519-537

Query Match 31.9%; Score 30; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy         12 LMPNIER 18
                :|||||:
Db          1 VMPNIEK 7
```

5204326-117
;Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
;INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
;METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
;SEQ ID NO:117:
; LENGTH: 9
5204326-117

S19-537

Query Match 34.0%; Score 32; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NLSSDIIG 8
              |||:|::|
Db          2 NLSTDVLG 9
```

```
Sequence 29, Application US/08447411
; Patent No. 5773243
;  GENERAL INFORMATION:
;    APPLICANT:  FRITZINGER, DAVID C.
;    APPLICANT:  BREDEHORST, REINHARD
;    APPLICANT:  VOGEL, CARL-WILHELM
;    TITLE OF INVENTION:  DNA ENCODING COBRA C3, CVF1, AND CVF2
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,411
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/043,747
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5773243man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1126-101-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-447-411-29

  Query Match             30.5%;  Score 32;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 KYELDK 15
              ||||||
Db          7 KYELDK 12
```

533-551

```
 Sequence 198, Application US/10658180
; Patent No. 6943002
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.DVUS02
;  CURRENT APPLICATION NUMBER: US/10/658,180
;  CURRENT FILING DATE:  2003-09-09
;  PRIOR APPLICATION NUMBER: US 09/755,630
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,669
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 295
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic polypeptide
US-10-658-180-198

  Query Match             28.6%;  Score 30;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 59;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YLRAQE 12
              ||||||
Db          1 YLRAQE 6
```

547 of 565

```
RESULT 13
Q9R3Y4_CLOPE
ID   Q9R3Y4_CLOPE   PRELIMINARY;   PRT;    23 AA.
AC   Q9R3Y4;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 14.
DE   Iota toxin component A (Fragment).
GN   Name=iap;
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=853, NCIB 10748, and 294;
RX   MEDLINE=98380411; PubMed=9712814;
RA   Billington S.J., Wieckowski E.U., Sarker M.R., Bueschel D.,
RA   Songer J.G., McClane B.A.;
RT   "Clostridium perfringens type E animal enteritis isolates with highly
RT   conserved, silent enterotoxin gene sequences.";
RL   Infect. Immun. 66:4531-4536(1998).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF037330; AAC34979.1; -; Genomic_DNA.
DR   EMBL; AF037328; AAC34977.1; -; Genomic_DNA.
DR   EMBL; AF037329; AAC34978.1; -; Genomic_DNA.
FT   NON_TER      23     23
SQ   SEQUENCE   23 AA;  2642 MW;  2DC67575E10BEC73 CRC64;

  Query Match             30.0%;  Score 30;  DB 2;  Length 23;
  Best Local Similarity   42.9%;  Pred. No. 3e+03;
  Matches    6;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 VKKVNKATEAAMFL 16
              :|||||:    : |
Db          1 MKKVNKSISVFLIL 14
```

Clm 93
589-607

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Sequence 41, Application US/08346455B
; Patent No. 5731167
;  GENERAL INFORMATION:
;    APPLICANT:  UNITED STATES OF AMERICA; DEPT.
;    APPLICANT:  OF HEALTH AND HUMAN SERVICES
;    TITLE OF INVENTION:  MOTILITY STIMULATING
;    TITLE OF INVENTION:  PROTEIN USEFUL IN CANCER DIAGNOSIS AND
;    TITLE OF INVENTION:  THERAPY
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  U.S.A.
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/346,455B
;      FILING DATE:  28-NOV-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/06613
;      FILING DATE:  24-MAY-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/249,182
;      FILING DATE:  25-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/822,043
;      FILING DATE:  17-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DOROTHY R. AUTH
;      REGISTRATION NUMBER:  36,434
;      REFERENCE/DOCKET NUMBER:  2026-4149PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7
;      TYPE:  amino acids
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  Peptide
;    HYPOTHETICAL:  No
;    FEATURE:
;      NAME/KEY:  ATX-209
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-08-346-455B-41

  Query Match             31.9%;  Score 30;  DB 1;  Length 7;
  Best Local Similarity   71.4%;  Pred. No. 5e+05;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
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519-537

```
Qy          12 LMPNIER 18
               :||||||:
Db           1 VMPNIEK 7
```

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RESULT 1
US-11-347-179-294
; Sequence 294, Application US/11347179
; Publication No. US20060178503A1
; GENERAL INFORMATION:
;  APPLICANT: LUNDGREN-AKERLUND, EVY
;  TITLE OF INVENTION: INTEGRIN HETERODIMER AND A SUBUNIT THEREOF
;  FILE REFERENCE: 034341-001
;  CURRENT APPLICATION NUMBER: US/11/347,179
;  CURRENT FILING DATE:  2006-02-06
;  PRIOR APPLICATION NUMBER: US/09/647,544
;  PRIOR FILING DATE: 2000-10-26
;  PRIOR APPLICATION NUMBER: PCT/SE99/00544
;  PRIOR FILING DATE: 1999-03-31
;  PRIOR APPLICATION NUMBER: SE 9900319.6
;  PRIOR FILING DATE: 1999-01-28
;  PRIOR APPLICATION NUMBER: SE 9801164-6
;  PRIOR FILING DATE: 1998-04-02
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 294
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-347-179-294

  Query Match             36.6%;  Score 34;  DB 7;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 LNESINK 9
              |||||||
Db          8 LNESINK 14
```

qq 771-789

```
RESULT 47
C85939
hypothetical protein Z4183 [imported] - Escherichia coli (strain O157:H7, substrain ED
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85939
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85939
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27
A;Cross-references: UNIPROT:Q8X3L8; UNIPARC:UPI00000D0EF5; GB:AE005174; NID:g12517358;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4183

  Query Match             21.6%;  Score 22;  DB 2;  Length 27;
  Best Local Similarity   66.7%;  Pred. No. 5.7e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NKFLNQ 6
              :|||:|
Db          8 DKFLSQ 13
```

ca 785-803

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RESULT 28
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ID   Q6EKS5_YERPE   PRELIMINARY;   PRT;    30 AA.
AC   Q6EKS5;
DT   16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT   16-AUG-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Hypothetical protein (Fragment).
OS   Yersinia pestis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Yersinia.
OX   NCBI_TaxID=632;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CIP 519/B2, CIP 548/B2, CIP 552/B3, CIP 557/B3, CIP 611/B4, CIP
RC   616/B4, CIP 685/B5, CIP CO92, and CIP 304;
RA   Roux V., Drancourt M., Raoult D.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY312300; AAQ94789.1; -; Genomic_DNA.
DR   EMBL; AY312301; AAQ94790.1; -; Genomic_DNA.
DR   EMBL; AY312302; AAQ94792.1; -; Genomic_DNA.
DR   EMBL; AY312303; AAQ94795.1; -; Genomic_DNA.
DR   EMBL; AY312304; AAQ94796.1; -; Genomic_DNA.
DR   EMBL; AY312305; AAQ94799.1; -; Genomic_DNA.
DR   EMBL; AY312306; AAQ94800.1; -; Genomic_DNA.
DR   EMBL; AY312307; AAQ94802.1; -; Genomic_DNA.
DR   EMBL; AY312299; AAQ94786.1; -; Genomic_DNA.
DR   InterPro; IPR007473; DUF519.
DR   Pfam; PF04378; DUF519; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   30 AA;  3417 MW;  F46332581AF6AC90 CRC64;

  Query Match             27.5%;  Score 28;  DB 2;  Length 30;
  Best Local Similarity   57.1%;  Pred. No. 7.1e+03;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 MNSMIPY 19
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Db          3 MNSLLPW 9
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785-803

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RESULT 28
US-10-946-371-33
; Sequence 33, Application US/10946371
; Publication No. US20050208587A1
; GENERAL INFORMATION:
;  APPLICANT: CARDOSO, ROSA
;  APPLICANT:  WILSON, IAN
;  APPLICANT:  BURTON, DENNIS
;  APPLICANT:  DAWSON, PHILIP
;  TITLE OF INVENTION: PEPTIDES THAT BIND TO BROADLY NEUTRALIZING ANTI-HIV
;  TITLE OF INVENTION:  ANTIBODY-STRUCTURE OF 4E10 FAB FRAGMENT COMPLEX, USES
;  TITLE OF INVENTION:  THEREOF, COMPOSITIONS THEREFROM
;  FILE REFERENCE: 678501-2001.1
;  CURRENT APPLICATION NUMBER: US/10/946,371
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: 60/504,123
;  PRIOR FILING DATE: 2003-09-19
;  PRIOR APPLICATION NUMBER: PCT/EP02/10070
;  PRIOR FILING DATE: 2002-09-09
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 33
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-10-946-371-33

  Query Match             35.7%;  Score 35;  DB 5;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TNWLAK 6
              ||||||
Db          9 TNWLAK 14
```

715-733

```
  d s
Set     Items   Description
S1       6814   S E2-E4
S2         71   S E2-E17
S3        916   S E41-E46
S4        175   'BOTULINUM TOXIN BTX':'BOTULINUM TOXIN C 2' OR E44-E48 FROM 155, 5, 34,
35, 45, 65, 71, 73, 91, 94, 98, 135, 144, 149, 156, 159, 162, 164, 172, 266, 369, 370,
399, 434, 444, 467
S5       7196   S S1 OR S2 OR S3 OR S4
S6     221938   'EPITOPE' FROM 155, 5, 34, 35, 45, 65, 71, 73, 91, 94, 98, 135, 144, 149,
156, 159, 162, 164, 172, 266, 369, 370, 399, 434, 444, 467
S7       4234   'MAPPING //EPITOPE'  (EPITOPE MAPPING) FROM 155, 5, 34, 35, 45, 65, 71,
73, 91, 94, 98, 135, 144, 149, 156, 159, 162, 164, 172, 266, 369, 370, 399, 434, 444, 467
È
S8         21   S S5 AND (S6 OR S7)
S9         20   RD  (unique items)

?  t s9/9/9 10 11 12 13-20
```

9/9/9 (Item 7 from file: 73) **Links**

EMBASE

11955596 **EMBASE No:** 2003066469

Overview of the needs and realities for developing new and improved vaccines in the 21st century

Hilleman M.R.

Dr. M.R. Hilleman, Merck Institute for Vaccinology, Merck and Co., Inc. (WP53C-350), 770 Sumneytown Pike, West Point, PA 19486 United States

Author Email: maurice hilleman@merck.com

Intervirology (INTERVIROLOGY) (Switzerland) 2002 , 45/4-6 (199-211)

CODEN: IVRYA **ISSN:** 0300-5526

Document Type: Journal ; Conference Paper

Language: ENGLISH **Summary Language:** ENGLISH

Number Of References: 90

The science of present day vaccinology is based on the pioneering discoveries of the late 18th and late 19th centuries and the technologic breakthroughs of the past 60 years. The driving force for the development of new vaccines resides in technologic feasibility, public need and economic incentive for translating the basic knowledge into a product. Past efforts by government to define which particular vaccines to develop were mostly irrelevant to the realistic choices which were made. There is a vast array of viral, bacterial, parasitic and fungal disease agents against which preventative vaccines may be developed, and to this may be added cancer and certain amyloidoses such as Alzheimer's and 'mad cow' diseases. The proven past for vaccines has relied on live, killed, protein and polysaccharide antigens plus the single example of recombinant-expressed hepatitis B vaccine. The validity of redirection of vaccinology to exploration of simplified vaccines such as recombinant vectored and DNA preparations and reductionist vaccines based on peptides of contrived **epitope** composition remains to be proved. Reductionism imposes vastly increased complexity and difficulty on vaccine development and might not be capable of achievement. The challenge in the 21st century will involve new and uncertain pathways toward worthwhile accomplishments. Copyright (c) 2003 S. Karger AG, Basel.

DRUG DESCRIPTORS:

* bacterial vaccine--drug development--dv; *virus vaccine--drug development --dv

hepatitis B vaccine; polysaccharide; antigen; DNA vaccine; diphtheria vaccine; tetanus toxoid; pertussis v

botulinum toxin A; Lyme disease vaccine; Pneumococcus vaccine; Meningococcus vaccine; influenza vaccine; BCG vaccine; typhoid vaccine; cholera vaccine; anthrax vaccine; poliomyelitis vaccine; measles vaccine; mumps vaccine; rubella vaccine; chickenpox vaccine; yellow fever vaccine; hepatitis A vaccine; rabies vaccine; Rotavirus vaccine; respiratory syncytial virus vaccine; parainfluenza vaccine; unindexed drug

MEDICAL DESCRIPTORS:

* vaccination; *bacterial infection--etiology--et; *bacterial infection --prevention--pc; *virus infection--etiology--et; *virus infection --prevention--pc

immune response; drug targeting; cancer immunization; amyloidosis; responsibility; government; Alzheimer disease; bovine spongiform encephalopathy; human; nonhuman; conference paper; priority journal

CAS Registry Number: 57425-69-1, 93384-51-1 (tetanus toxoid); 93384-43-1 (**botulinum toxin A**)

Section Headings:

004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
008 Neurology and Neurosurgery
016 Cancer
026 Immunology, Serology and Transplantation
037 Drug Literature Index

9/9/10 (Item 8 from file: 73) **Links**
EMBASE

11542312 **EMBASE No:** 2002114797

Characterisation of monoclonal antibodies against haemagglutinin associated with Clostridium botulinum type C neurotoxin

Mahmut N.; Inoue K.; Fujinaga Y.; Hughes L.; Arimitsu H.; Sakaguchi Y.; Ohtsuka A.; Murakami T.; Yokota K.; Oguma K.
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Author Email: kuma@md.okayama-u.ac.jp
Journal of Medical Microbiology (J. MED. MICROBIOL.) (United Kingdom) 2002 , 51/4 (286-294)
CODEN: JMMIA **ISSN:** 0022-2615
Document Type: Journal ; Article
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 12

Of 11 monoclonal antibodies (MAbs) prepared against the non-toxic component of type C Clostridium botulinum 16S toxin to clarify the function of the non-toxic component, seven recognised HA1, three recognised HA3b and one recognised HA2. Results of **epitope** mapping indicated that three of the seven anti-HA1 MAbs recognised the region between amino acid residues 121 and 140 and four recognised the three-dimensional structure of HA1. Three anti-HA3b MAbs recognised different regions between (approximately) amino acids 405-430, 180-270 and 275-297. The ability of these MAbs to interfere with binding of 16S toxin or non-toxic component, HA1 or HA3b to erythrocytes and to intestine tissue sections of guinea-pig was observed. MAbs against HA3b and HA2 did not inhibit 16S toxin binding to either erythrocytes or epithelial cells, whereas some MAbs against HA1 did inhibit binding. The seven anti-HA1 MAbs can be classified into four groups based on their binding inhibition activities. The anti-HA1 MAbs that inhibited the binding of 16S toxin to the epithelial cells also neutralised or reduced the oral toxicity in mice, indicating that HA may play an important role in the absorption of the 16S toxin from the small intestine.

DRUG DESCRIPTORS:
* monoclonal antibody; *hemagglutinin--endogenous compound--ec; *neurotoxin --drug toxicity--to; *neurotoxin--endogenous compound--ec; *botulinum toxin --drug toxicity--to; *botulinum toxin--endogenous compound--ec
amino acid--endogenous compound--ec; neutralizing antibody; unclassified drug
MEDICAL DESCRIPTORS:
* Clostridium botulinum; *protein function
epitope mapping; antibody structure; antigen binding; inhibition kinetics; binding site; molecular recognition; erythrocyte; epithelium cell ; intestine epithelium; guinea pig; toxin analysis; intestine absorption; nonhuman; female; mouse; animal experiment; animal tissue; animal cell; article; priority journal
Drug Terms (Uncontrolled): botulinum toxin c--drug toxicity--to; **botulinum toxin c** --endogenous compound--ec
CAS Registry Number: 37333-12-3 (hemagglutinin); 39386-17-9 (neurotoxin); 65072-01-7 (amino acid)
Section Headings:
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
026 Immunology, Serology and Transplantation

9/9/11 (Item 9 from file: 73) **Links**
EMBASE

11505346 **EMBASE No:** 2002076810

Genetic and immunological comparison of anti-botulinum type A antibodies from immune and non-immune human phage libraries

Amersdorfer P.; Wong C.; Smith T.; Chen S.; Deshpande S.; Sheridan R.; Marks J.D.
P. Amersdorfer, Department of Biology, Corvas International, 3030 Science Park Road, San Diego, CA 92121 United States
Author Email: peter amersdorfer@corvas.com
Vaccine (VACCINE) (United Kingdom) 22 FEB 2002 , 20/11-12 (1640-1648)
CODEN: VACCD **ISSN:** 0264-410X
Publisher Item Identifier: S0264410X01004820
Document Type: Journal ; Article
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 44

Understanding the antibody response in botulinum intoxication is important for vaccine design and passive prophylaxis. To investigate this activity, we have studied the immune response to BoNT/A (botulinum neurotoxin serotype A) binding domain (HSUBC) at the molecular level using phage display. The scFv antibodies were isolated from V-gene repertoires prepared from (a) human volunteer immunized with pentavalent botulinum toxoid and (b) non-immune human peripheral blood lymphocytes and spleenocytes. A large panel of serotype specific phage expressing botulinum binding scFv could be selected from both libraries. **Epitope** mapping of immune scFv binders towards BoNT/A HSUBC revealed surprisingly a limited number of scFv recognizing conformational epitopes that corresponded to two distinct groups, clusters I and II. Only scFv from cluster I exhibited neutralizing activity in the mouse hemidiaphragm assay. Anti- BoNT/A HSUBC clones derived from a non-immune library could be conveniently grouped into clusters III-XI and appeared to share no overlapping epitopes with cluster I or II. In addition they showed no neutralization of toxin at biologically significant concentrations. We therefore suggest that a vaccine based on the pentavalent botulinum toxoid directs the humoral immune response to a limited number of immunodominant epitopes exposed on the binding domain HSUBC. (c) 2002 Elsevier Science Ltd. All rights reserved.

DRUG DESCRIPTORS:
*** botulinum toxin A**--pharmacology--pd; ***epitope**--pharmacology --pd; *single chain fragment variable antibody--drug comparison--cm; * single chain fragment variable antibody--pharmacology--pd; *neutralizing antibody--drug comparison--cm; *neutralizing antibody--pharmacology--pd; * vaccine--drug comparison--cm; *vaccine--pharmacology--pd
botulinum toxin--pharmacology--pd; unclassified drug
MEDICAL DESCRIPTORS:
* botulism--etiology--et; *antibody library
phage display; immune response; antibody isolation; immunization; binding site; lymphocyte; spleen cell; serotype; bacteriophage; protein expression; **epitope** mapping; antigen binding; antigen recognition; antibody combining site; drug activity; hemidiaphragm; vaccine production; humoral immunity; nonhuman; male; mouse; animal model; controlled study; animal tissue; article; priority journal
Drug Terms (Uncontrolled): botulinum toxin a antibody--drug comparison--cm; botulinum toxin a antibody --pharmacology--pd

CAS Registry Number: 93384-43-1 (**botulinum toxin A**); 334577-34-3, 334577-38-7 (single chain fragment variable antibody)
Section Headings:
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
026 Immunology, Serology and Transplantation
037 Drug Literature Index

9/9/12 (Item 10 from file: 73) **Links**
EMBASE

11319442 **EMBASE No:** 2001333655
Epitope mapping of neutralizing botulinum neurotoxin A antibodies by phage display

Mullaney B.P.; Pallavicini M.G.; Marks J.D.
B.P. Mullaney, UCSF Cancer Center, Box 0808, UCSF, San Francisco, CA 94143-0808 United States
Author Email: mullaney@cc.ucsf.edu
Infection and Immunity (INFECT. IMMUN.) (United States) 2001 , 69/10 (6511-6514)
CODEN: INFIB **ISSN:** 0019-9567
Document Type: Journal ; Article
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 27

Single-chain antibodies neutralize activity and bind nonoverlapping epitopes of botulinum A neurotoxin. Two phage display **epitope** libraries were constructed from the 1.3 kb of binding domain cDNA. The minimal epitopes selected against the single-chain Fv-Fc antibodies correspond to conformational epitopes with amino acid residues 1115 to 1223 (S25), 1131 to 1264 (3D12), and 889 to 1294 (C25).

Molecular Sequence Number: ; GENBANK, U22962
DRUG DESCRIPTORS:
* **epitope**; ***botulinum toxin A**; *neutralizing antibody; *Fc receptor
MEDICAL DESCRIPTORS:
* gene mapping; *Clostridium botulinum; *nucleotide sequence
bacteriophage; antigen binding; DNA library; protein domain; amino acid sequence; protein conformation; drug receptor binding; gel electrophoresis; DNA sequence; molecular model; crystal structure; article; priority journal
CAS Registry Number: 93384-43-1 (**botulinum toxin A**)
Section Headings:
026 Immunology, Serology and Transplantation
029 Clinical and Experimental Biochemistry

9/9/13 (Item 11 from file: 73) **Links**
EMBASE

10973449 **EMBASE No:** 2001017400

Light chain of botulinum a neurotoxin expressed as an inclusion body from a synthetic gene is catalytically and functionally active

Ahmed S.A.; Smith L.A.
L.A. Smith, Dept. of Immunol. and Molec. Biology, Toxinology Division, U.S. Army Medical Research Institute, 1425 Porter Street, Fort Detrick, MD 21702 United States
Author Email: leonard.smith@amedd.army.mil
Journal of Protein Chemistry (J. PROTEIN CHEM.) (United States) 2000 , 19/6 (475-487)
CODEN: JPCHD **ISSN:** 0277-8033
Document Type: Journal ; Article
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 46

Botulinum neurotoxins, the most potent of all toxins, induce lethal neuromuscular paralysis by inhibiting exocytosis at the neuromuscular junction. The light chains (LC) of these dichain neurotoxins are a new class of zinc-endopeptidases that specifically cleave the synaptosomal proteins, SNAP-25, VAMP, or syntaxin at discrete sites. To facilitate the structural and functional characterization of these unique endopeptidases, we constructed a synthetic gene for the LC of the botulinum neurotoxin serotype A (BoNT/A), overexpressed it in Escherichia coli, and purified the gene product from inclusion bodies. Our procedure can provide 1.1 g of the LC from 1 L of culture. The LC product was stable in solution at 4degreesC for at least 6 months. This rBoNT/A LC was proteolytically active, specifically cleaving the Glu-Arg bond in a 17-residue synthetic peptide of SNAP-25, the reported cleavage site of BoNT/A. Its calculated catalytic efficiency kSUBcat/KSUBm was higher than that reported for the native BoNT/A dichain. Treating the rBoNT/A LC with mercuric compounds completely abolished its activity, most probably by modifying the cysteine-164 residue located in the vicinity of the active site. About 70% activity of the LC was restored by adding ZnSUP2+ to a ZnSUP2+ - free, apo-LC preparation. The LC was nontoxic to mice and failed to elicit neutralizing **epitope**(s) when the animals were vaccinated with this protein. In addition, injecting rBoNT/A LC into sea urchin eggs inhibited exocytosis-dependent plasma membrane resealing. For the first time, results of our study make available a large amount of the biologically active toxin fragment in a soluble and stable form.

DRUG DESCRIPTORS:
* **botulinum toxin A**--drug toxicity--to
neurotoxin--drug toxicity--to
MEDICAL DESCRIPTORS:
* neurotoxicity--etiology--et; *cell inclusion; *neuromuscular synapse paralysis--etiology--et; toxin analysis; exocytosis; peptide analysis; Escherichia coli; gene expression; vaccination; nonhuman; male; mouse; animal experiment; article
CAS Registry Number: 93384-43-1 (**botulinum toxin A**); 39386-17-9 (neurotoxin)
Section Headings:
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
008 Neurology and Neurosurgery
026 Immunology, Serology and Transplantation
052 Toxicology

9/9/14 (Item 12 from file: 73) **Links**
EMBASE

10971923 **EMBASE No:** 2001015519

High-affinity, protective antibodies to the binding domain of botulinum neurotoxin type A

Pless D.D.; Torres E.R.; Reinke E.K.; Bavari S.
S. Bavari, Dept. of Cell Biology/Biochemistry, U.S. Army Med. Res. Inst. Inf. Dis., 1425 Porter St., Frederick, MD 21702-5011 United States
Author Email: Sina.Bavari@AMEDD.Army.Mil
Infection and Immunity (INFECT. IMMUN.) (United States) 2001 , 69/1 (570-574)
CODEN: INFIB **ISSN:** 0019-9567
Document Type: Journal ; Article
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 19

Monocionai antibodies (MAbs) were prepared against the putative binding domain of botulinum neurotoxin A (BoNT/A), a nontoxic 50-kDa fragment. Initially, all fusion products were screened against the holotoxin BoNT/A and against the binding fragment, BoNT/A HSUBC. Eleven neutralizing hybridomas were cloned, and their specific binding to BoNT/A HSUBC was demonstrated by surface plasmon resonance, with dissociation constants ranging from 0.9 to <0.06 nM. **Epitope** mapping by real-time surface plasmon resonance showed that the antibodies bound to at least two distinct regions of the BoNT/A HSUBC fragment. These MAbs will be useful tools for studying BoNT/A interactions with its receptor, and they have potential diagnostic and therapeutic applications.

DRUG DESCRIPTORS:
* **botulinum toxin A**; *monoclonal antibody--intraperitoneal drug administration--ip
MEDICAL DESCRIPTORS:
* antibody production; *antigen binding
binding site; hybridoma; **epitope** mapping; dissociation constant; molecular interaction; kinetics; nonhuman; mouse; animal experiment; controlled study; animal cell; article; priority journal
CAS Registry Number: 93384-43-1 (**botulinum toxin A**)
Section Headings:
026 Immunology, Serology and Transplantation
037 Drug Literature Index

9/9/15 (Item 13 from file: 73) **Links**
EMBASE

10894888 **EMBASE No:** 2000379437

Anomalous enhancement of botulinum toxin type A neurotoxicity in the presence of antitoxin

Sheridan R.E.; Deshpande S.S.; Amersdorfer P.; Marks J.D.; Smith T.
R.E. Sheridan, Neurotoxicology Branch, Pharmacology Division, US Army Medical Research Institute, 3100 Ricketts Point Road, Aberdeen Proving Ground, MD 21010 United States
Author Email: robert.sheridan@amedd.army.mil
Toxicon (TOXICON) (United Kingdom) 2001 , 39/5 (651-657)
CODEN: TOXIA **ISSN:** 0041-0101
Publisher Item Identifier: S0041010100001896
Document Type: Journal ; Article
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 13

The neutralization of botulinum toxin serotype A with polyclonal equine antitoxin was studied in isolated mouse hemidiaphragms and compared to the same action in live mice. The biological activity of the toxin in the isolated muscle could be markedly reduced with excess antitoxin, estimated as 3:1 molar ratios of IgG Ab:toxin or better. Toxin neutralization in vivo required higher ratios of Ab:toxin, ranging from 30:1 at high toxin doses and increasing to 100:1 at 10xLD50 toxin. At equimolar Ab to toxin ratios in the isolated muscle, the biological activity of the toxin underwent a statistically significant increase. This paradoxical effect of the polyclonal antisera was serotype selective and independent of the presence or absence of hemagglutinin in the toxin. The enhancement of toxin activity was subsequently localized to occupancy of one of four epitopes on the toxin using monoclonal antibodies to mimic the effect of the antitoxin. The enhancement of toxin activity suggests that botulinum toxin may undergo a conformational change upon binding antibodies to certain domains. This phenomenon could contribute to the observed concentration dependent changes in neutralization efficacy with antitoxin in vivo. Copyright (C) 2000 .

DRUG DESCRIPTORS:
* **botulinum toxin A**--drug toxicity--to; *antitoxin--pharmacology--pd; *neurotoxin--drug toxicity--to **epitope**; hemagglutinin--endogenous compound--ec; cell surface receptor--endogenous compound--ec; monoclonal antibody--pharmacology--pd

MEDICAL DESCRIPTORS:
* neurotoxicity--etiology--et; *botulism--etiology--et; *toxicity testing
drug activity; nonhuman; male; mouse; animal experiment; animal model; controlled study; animal tissue; article; priority journal

CAS Registry Number: 93384-43-1 (**botulinum toxin A**); 39386-17-9 (neurotoxin); 37333-12-3 (hemagglutinin)
Section Headings:
037 Drug Literature Index
052 Toxicology
008 Neurology and Neurosurgery

infection--epidemiology--ep; human; nonhuman; conference paper; priority journal
CAS Registry Number: 93384-43-1 (**botulinum toxin A**); 39386-17-9 (neurotoxin)
Section Headings:
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
008 Neurology and Neurosurgery
037 Drug Literature Index
052 Toxicology

9/9/17 (Item 15 from file: 73) **Links**
EMBASE

07757198 **EMBASE No:** 1999241087
Structure, activity, and immune (T and B cell) recognition of botulinum neurotoxins

Atassi M.Z.; Oshima M.
M.Z. Atassi, Department of Biochemistry, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030 United States
Critical Reviews in Immunology (CRIT. REV. IMMUNOL.) (United States) 1999 , 19/3 (219-260)
CODEN: CCRID **ISSN:** 1040-8401
Document Type: Journal ; Review
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 271

Botulism, which was first reported over a century ago, is caused by botulinum neurotoxins produced by Clostridium botulinum in seven immunological serotypes (A through G). The primary structures of a number of these BoNTs have been determined and are reviewed here, together with their gene structure and synthesis. The biological actions of BoNTs, which result in their ability to block neurotransmitter release have been the subject of intensive study, and in this review we discuss the binding of BoNTs to the cell surface as well as the mechanism of their intercellular action. The ability of BoNTs to block neurotransmitter release has been exploited in therapeutic applications to reduce muscle hyperactivity for the treatment of a variety of clinical conditions associated with involuntary muscle spasm and contractions. The advantages, limitations, and risks of these applications are discussed. Certain compounds provide some limited protection against BoNT. However, more effective protection has been obtained immunologically either by passive immunity (i.e., by administration of anti-BoNT Abs) or by immunization with inactivated toxin. More recently, excellent protection has been obtained by immunization with the receptor-binding region comprising the C-terminal (residues 860 to 1296) fragment (H(C)) of the heavy chain of BoNT/A. Here we review the mapping of the epitopes on the Hc region of BoNT/A that are recognized by anti-BoNT/A Abs raised in horse, human, and mouse. The epitopes on the H(C) that are recognized by anti-H(C) Abs and by H(C)-primed T lymphocytes were mapped in two mouse strains [BALB/c (H-2(d)) and SJL (H- 2(s))]. The peptides, which contain Ab or T cell epitopes (or both) on the H(C), were used as immunogens in BALB/c and SJL mice and we identified those peptides whose Ab and/or T-cell responses cross-react with H(C). Identification of these peptides is an important first step in the intricate requirements for the design of a synthetic vaccine.

DRUG DESCRIPTORS:
*** botulinum toxin a**; *neurotransmitter--endogenous compound--ec; * inactivated vaccine--drug therapy--dt; ***epitope**--endogenous compound --ec
MEDICAL DESCRIPTORS:
* antigen recognition; *t lymphocyte; *b lymphocyte
botulism--drug therapy--dt; botulism--prevention--pc; gene structure; neurotransmitter release; passive immunization; carboxy terminal sequence; cross reaction; human; nonhuman; mouse; review; priority journal
CAS Registry Number: 93384-43-1 **(botulinum toxin a)**
Section Headings:
026 Immunology, Serology and Transplantation
037 Drug Literature Index

9/9/18 (Item 16 from file: 73) **Links**
EMBASE

07203386 **EMBASE No:** 1998096328

Antibodies and T cells against synthetic peptides of the C-terminal domain (H(c)) of botulinum neurotoxin type A and their cross-reaction with H(c)

Oshima M.; Middlebrook J.L.; Atassi M.Z.
M.Z. Atassi, Department of Biochemistry, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030 United States
Author Email: matassi@bcm.tmc.edu
Immunology Letters (IMMUNOL. LETT.) (Netherlands) 1998 , 60/1 (7-12)
CODEN: IMLED **ISSN:** 0165-2478
Publisher Item Identifier: S0165247897001247
Document Type: Journal ; Article
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 21

Seventeen peptides containing T cell and/or antibody (Ab) epitopes previously localized on H(c) of botulinum neurotoxin type A were used in SJL and BALB/c mice as immunogens either individually or as an equimolar mixture of groups that contained epitopes of T cells, Abs or both, to determine their abilities to generate T cells and/or Abs that recognize intact H(c). In SJL, peptide 897-915 which included both T cell and Ab epitopes, elicited Abs that cross-reacted very strongly with H(c). In BALB/c, peptides 869-887, 883-901, 981-999 and 1275-1296 which contained Ab epitopes generated Abs that cross- reacted strongly with H(c). A mixture of peptides that contained T cell and Ab epitopes was effective in both strains in eliciting T cells and Abs that cross-reacted with H(c). This mixture form gave a quicker rise (after two injections) in cross-reactive (with H(c)) Ab titer as compared to other peptide mixtures or the individual peptides, and sustained in BALB/c a high Ab titer upon further booster injections. Some of the regions that elicited crossreactive immunity to H(c) have sequence similarity to other clostridial toxins, suggesting that one or more of these synthetic peptides might provide cross-protection against those toxins.

DRUG DESCRIPTORS:
* **botulinum toxin a**; *synthetic peptide--drug development--dv; * bacterial vaccine--drug development--dv neurotoxin; **epitope**; cross reacting antibody
MEDICAL DESCRIPTORS:
* botulism--etiology--et; *botulism--prevention--pc; *t lymphocyte; * immunization neurotoxicity--etiology--et; neurotoxicity--prevention--pc; lymph node cell ; lymphocyte proliferation; peptide synthesis; cross reaction; antibody titer; clostridium botulinum; nonhuman; mouse; animal model; animal cell; subcutaneous drug administration; article; priority journal
CAS Registry Number: 93384-43-1 (**botulinum toxin a**); 39386-17-9 (neurotoxin)
Section Headings:
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
026 Immunology, Serology and Transplantation
037 Drug Literature Index

9/9/19 (Item 17 from file: 73) **Links**
EMBASE

07000286 **EMBASE No:** 1997286617

Molecular characterization of murine humoral immune response to botulinum neurotoxin type A binding domain as assessed by using phage antibody libraries

Amersdorfer P.; Wong C.; Chen S.; Smith T.; Deshpande S.; Sheridan R.; Finnern R.; Marks J.D.
J.D. Marks, University of California, San Francisco General Hospital, 1001 Potrero Ave., San Francisco, CA 94110 United States
Infection and Immunity (INFECT. IMMUN.) (United States) 1997 , 65/9 (3743-3752)
CODEN: INFIB **ISSN:** 0019-9567
Document Type: Journal ; Article
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 51

To produce antibodies capable of neutralizing botulinum neurotoxin type A (BoNT/A), the murine humoral immune response to BoNT/A binding domain (H(C)) was characterized at the molecular level by using phage antibody libraries. Mice were immunized with BoNT/A H(C), the spleens were harvested, and single-chain Fv (scFv) phage antibody libraries were constructed from the immunoglobulin heavy and light chain variable region genes. Phage expressing BoNT/A binding scFv were isolated by selection on immobilized BoNT/A and BoNT/A H(C). Twenty-eight unique BoNT/A H(C) binding scFv were identified by enzyme-linked immunosorbent assay and DNA sequencing. **Epitope** mapping using surface plasmon resonance in a BIAcore revealed that the 28 scFv bound to only 4 nonoverlapping epitopes with equilibrium constants (K(d)) ranging from 7.3 x 10sup - sup 8 to 1.1 x 10sup -sup 9 M. In a mouse hemidiaphragm assay, scFv binding epitopes 1 and 2 significantly prolonged the time to neuroparalysis, 1.5- and 2.7-fold, respectively, compared to toxin control. scFv binding to epitopes 3 and 4 showed no protection against neuroparalysis. A combination of scFv binding epitopes 1 and 2 had an additive effect on time to neuroparalysis, which increased to 3.9-fold compared to the control. The results suggest that there are two 'productive' receptor binding sites on H(C) which lead to toxin internalization and toxicity. Blockade of these two epitopes with monoclonal antibodies may provide effective immunoprophylaxis or therapy against BoNT/A intoxication.

DRUG DESCRIPTORS:
*** botulinum toxin a**
MEDICAL DESCRIPTORS:
* binding site; *humoral immunity
antibody production; article; bacteriophage; dna library; immunization; immunoprophylaxis; internalization; molecular genetics; nonhuman; phage display; priority journal
CAS Registry Number: 93384-43-1 **(botulinum toxin a)**
Section Headings:
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology

9/9/20 (Item 18 from file: 73) Links
EMBASE

06853948 **EMBASE No:** 1997136549

Antibody mapping to domains of botulinum neurotoxin serotype A in the complexed and uncomplexed forms

Chen F.; Kuziemko G.M.; Amersdorfer P.; Wong C.; Marks J.D.; Stevens R.C.
J.D. Marks, Anesthesia/Pharmaceut. Chem. Dept., University of California, SFGH, 1001 Potrero, San Francisco, CA 94110 United States
Infection and Immunity (INFECT. IMMUN.) (United States) 1997 , 65/5 (1626-1630)
CODEN: INFIB **ISSN:** 0019-9567
Document Type: Journal ; Article
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 28

The domain organization of the botulinum neurotoxin serotype A was studied by using antibody mapping of 44 monoclonal single-chain variable fragments. The analysis was carried out on (i) the individual domains of botulinum neurotoxin holotoxin (binding, translocation, and catalytic), (ii) botulinum neurotoxin holotoxin, (iii) the botulinum neurotoxin holotoxin in complex with the nontoxic portion, and (iv) botulinum neurotoxin holotoxin and nontoxic portion of the complex recombined in vitro. All 44 antibodies mapped to individual domains of botulinum neurotoxin. Forty of the 44 single-chain variable fragments bound the botulinum neurotoxin holotoxin relative to the isolated domains, suggesting that 4 epitopes are covered when the individual domains are in the holotoxin form. Only 20 of the antibodies showed a positive reaction to the toxin while in complex with the nontoxic portion. All of the covered epitopes were mapped to the binding domain of botulinum neurotoxin, which suggested that the binding domain is in direct contact with the nontoxic portion in the complex. Based on the antibody mapping to the different domains of the botulinum neurotoxin holotoxin and the entire complex, a model of the botulinum neurotoxin complex is proposed.

DRUG DESCRIPTORS:
* **botulinum toxin a**--endogenous compound--ec
epitope
MEDICAL DESCRIPTORS:
* botulism--etiology--et; *clostridium botulinum
antigen antibody complex; antigen recognition; article; nonhuman; priority journal; serotype; toxin analysis
CAS Registry Number: 93384-43-1 (**botulinum toxin a**)
Section Headings:
004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
026 Immunology, Serology and Transplantation

9/9/16 (Item 14 from file: 73) **Links**
EMBASE

10594483 **EMBASE No:** 2000060235

Botulism: Laboratory methods and epidemiology

Fernandez R.A.; Ciccarelli A.S.
R.A. Fernandez, Catedra de Microbiologia, Facultad de Ciencias Medicas, Universidad Nacional de Cuyo, Casilla de Correo 33, (5500) Mendoza Argentina
Author Email: rfernand@fmed2.uncu.edu.ar
Anaerobe (ANAEROBE) (United Kingdom) 1999 , 5/3-4 (165-168)
CODEN: ANAEF **ISSN:** 1075-9964
Document Type: Journal ; Conference Paper
Language: ENGLISH **Summary Language:** ENGLISH
Number Of References: 27

Although food botulism (FB) in Argentina was described by 1911, the first documented outbreak was recorded in 1922. In 1957, an outbreak of type A FB caused by red bell peppers was the first laboratory confirmation of botulism in Argentina. From 1922 to 1997, 70 FB outbreaks affecting 242 persons with 111 deaths (case fatality rate, 46%) were reported in Argentina. Infant botulism (IB) was recognized in 1976 and has been mostly diagnosed in the U.S.A. More than 146 IB cases have been reported in Argentina since 1982. Additional cases may go undiagnosed due to physician inexperience and limited access to diagnostic services. A single laboratory-confirmed case of wound botulism (WB) occurred in Argentina in 1995. The botulinal neurotoxins (BoNTs) identified in Argentina have been types A, B, E, F and Af in FB, and exclusively type A in IB and WB. For the laboratory diagnosis of botulism, serum, gastrointestinal sample, food, and wounds should be tested for BoNT. Gastrointestinal, wound and food sample must also be cultured for toxigenic organisms. When higher volumes of serum were tested, BoNT was found in 61% of IB patients in Mendoza compared with 13% in a previous series from the U.S.A. Reliable typing can only be achieved when the BoNT belongs to a known serotype and the toxin titer is above 4000 LDinf 5inf 0/mL. When these criteria are not met, as in most clinical samples, bacterial isolation, purification and adequate toxin production in culture are required. Neutralization testing must be performed at not less than three 10-fold doses of toxin because of (1) the existence of subtypes, where a second, minor serotype is present, (2) the sharing of epitopes between certain serotypes, and (3) the occurrence of serological variants. Three basic properties of working antitoxins, specificity, protency and avidity, must be known for BoNT typing. The efficiency index (EI), which expresses the avidity of antitoxins, is an important instrument for recognizing BoNT subtypes. (C) 1999 Academic Press.

DRUG DESCRIPTORS:
antibiotic agent--drug therapy--dt; antitoxin--drug therapy--dt; **botulinum toxin A**--endogenous compound--ec; **botulinum toxin B** --endogenous compound--ec; **epitope**--endogenous compound--ec; neurotoxin--endogenous compound--ec

MEDICAL DESCRIPTORS:
* botulism--complication--co; *botulism--diagnosis--di; *botulism--drug therapy--dt; *botulism--epidemiology--ep Argentina; Clostridium botulinum; LD 50; United States; bacterium isolation ; food analysis; food poisoning--diagnosis--di; food poisoning--drug therapy--dt; food poisoning--epidemiology--ep; gastrointestinal tract; infant disease--diagnosis--di; infant disease--drug therapy--dt; infant disease--epidemiology--ep; laboratory diagnosis; mortality; pepper; purification; sampling; serotype; titrimetry; toxin synthesis; wound infection--complication--co; wound infection--diagnosis--di; wound infection--drug therapy--dt; wound

052 Toxicology

615	22	23.4	25	2	Q56C76_9HIV1	Q56c76	human immun
616	22	23.4	25	2	Q56C77_9HIV1	Q56c77	human immun
617	22	23.4	25	2	Q56C78_9HIV1	Q56c78	human immun
618	22	23.4	25	2	Q56C79_9HIV1	Q56c79	human immun
619	22	23.4	25	2	Q71940_9HIV1	Q71940	human immun
620	22	23.4	25	2	Q71946_9HIV1	Q71946	human immun
621	22	23.4	25	2	Q8QE38_9HIV1	Q8qe38	human immun
622	22	23.4	25	2	Q9IQQ5_9HIV1	Q9iqq5	human immun
623	22	23.4	26	1	MEL_APIFL	P01504	apis florea
624	22	23.4	26	1	MGN_CHICK	P50594	gallus gall
625	22	23.4	26	1	RBL_VICFA	P05699	vicia faba
626	22	23.4	26	2	Q4XDG9_PLACH	Q4xdg9	plasmodium
627	22	23.4	26	2	Q4XIE0_PLACH	Q4xie0	plasmodium
628	22	23.4	26	2	Q4XM72_PLACH	Q4xm72	plasmodium
629	22	23.4	26	2	Q4XMQ5_PLACH	Q4xmq5	plasmodium
630	22	23.4	26	2	Q4XRY4_PLACH	Q4xry4	plasmodium
631	22	23.4	26	2	Q4YT83_PLABE	Q4yt83	plasmodium
632	22	23.4	26	2	Q4Z6G9_PLABE	Q4z6g9	plasmodium
633	22	23.4	26	2	Q9T0Q6_LAMBD	Q9t0q6	bacteriopha
634	22	2					

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_813_831
Perfect score: 94
Sequence: 1 ASLKDALLKYIYDNRGTLI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94	100.0	19	9	ADW11067	Adw11067 Clostridi
2	94	100.0	27	9	ADW11117	Adw11117 Clostridi
3	47	50.0	27	9	ADW11118	Adw11118 Clostridi
4	38	40.4	30	9	AEC96081	Aec96081 TccC3 fra
5	38	40.4	30	9	AEC96090	Aec96090 TccC3 fra
6	38	40.4	30	9	AEC96094	Aec96094 TccC3 fra
7	38	40.4	30	9	AEC96087	Aec96087 TccC3 fra
8	38	40.4	30	9	AEC96084	Aec96084 TccC3 fra
9	36	38.3	17	7	ADE01171	Ade01171

```
RESULT 43
US-08-213-124-9
; Sequence 9, Application US/08213124
; Patent No. 5693325
; GENERAL INFORMATION:
;    APPLICANT:  Kahn, Michael
;    TITLE OF INVENTION:  PEPTIDE VACCINES AND METHODS RELATING
;    TITLE OF INVENTION:  THERETO
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/213,124
;      FILING DATE:  15-MAR-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hermanns, Karl R.
;      REGISTRATION NUMBER:  33,507
;      REFERENCE/DOCKET NUMBER:  670063.411
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;      TELEX:  3723836 SEEDANDBERRY
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-213-124-9

  Query Match             30.9%;  Score 29;  DB 1;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 3.6e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 DNRGTLI 19
              |:|||:|
Db          7 DHRGTII 13
```

```
RESULT 1
H64640
hypothetical protein HP0968 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: H64640
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: H64640
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-21
A;Cross-references: UNIPROT:O25621; UNIPARC:UPI00000C07B7; GB:AE000605; GB:AE000511; N

  Query Match             33.0%;  Score 31;  DB 2;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 LKDALLKY 10
              |||||: |
Db         12 LKDALIDY 19
```

```
RESULT 12
Q8ZL14_SALTY
ID   Q8ZL14_SALTY   PRELIMINARY;   PRT;    29 AA.
AC   Q8ZL14;
DT   01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2002, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Conserved protein in the LexA regulon.
GN   Name=ysdB; OrderedLocusNames=STM3797.2; ORFNames=STM3796B;
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AE008877; AAL22656.1; -; Genomic_DNA.
DR   BioCyc; STYP99287:STM3796B-MONOMER; -.
KW   Complete proteome.
SQ   SEQUENCE   29 AA;  3211 MW;  9A3B645EB233E781 CRC64;

  Query Match             33.0%;  Score 31;  DB 2;  Length 29;
  Best Local Similarity   66.7%;  Pred. No. 2.6e+03;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 LKDALLKYI 11
              | ||:|||:
Db         20 LLDAVLKYL 28
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_981_999
Perfect score: 98
Sequence: 1 GEIIWTLQDTQEIKQRVVF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	98	100.0	19	9	ADW11079	Adw11079 Clostridi
2	74	75.5	19	9	ADZ69820	Adz69820 Botulinum
3	40	40.8	19	7	ADF14824	Adf14824 SLE/sjogr
4	38	38.8	15	6	ABR38942	Abr38942 HPV-16 E2
5	37.5	38.3	14	4	ABB56643	Abb56643 Human SNP
6	36	36.7	12	2	AAR91293	Aar91293 Anti-idio
7	36	36.7	15	6	ABR38932	Abr38932 HPV-11 E2
8	36	36.7	15	9	AEC98599	Aec98599 HLA-DR bi
9	36	36.7	15	9	AEC98632	Aec98632 HLA-DR bi

```
RESULT 4
ABR38942
ID   ABR38942 standard; protein; 15 AA.
XX
AC   ABR38942;
XX
DT   10-MAY-2003  (first entry)
XX
DE   HPV-16 E2 transactivation domain peptide fragment # SEQ ID 22.
XX
KW   Transactivation domain; HPV-11; E2 protein; TAD-inhibitor complex;
KW   binding.
XX
OS   Human papillomavirus.
XX
PN   WO2003006495-A2.
XX
PD   23-JAN-2003.
XX
PF   12-JUL-2002; 2002WO-CA001058.
XX
PR   12-JUL-2001; 2001US-0304412P.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (WANG/) WANG Y.
XX
PI   Cameron DR,  Archambault J,  Yoakim C,  White P;
XX
DR   WPI; 2003-239235/23.
XX
PT   Crystallizable composition comprising papilloma virus E2 transactivation
PT   domain-like polypeptide, complexed with an inhibitor, useful for
PT   providing information about inhibitor-binding pocket of transactivation
PT   domain.
XX
PS   Disclosure; Fig 10; 83pp; English.
XX
CC   The invention relates to a crystallizable composition, comprising a
CC   papilloma virus (PV) E2 transactivation domain (TAD)-like polypeptide
CC   complexed with an inhibitor. Compositions of the invention are useful for
CC   providing useful information on the inhibitor-binding pocket of the
CC   transactivation domain of the HPV-E2 protein. The HPV E2 TAD-inhibitor
CC   crystal structure can be used to identify the residues which are members
CC   of the HPV inhibitor binding pocket and which differ in the CRPV protein.
CC   The current sequence represents the HPV-16 E2 transactivation domain
CC   inhibitor-binding pocket peptide
XX
SQ   Sequence 15 AA;

  Query Match             38.8%;  Score 38;  DB 6;  Length 15;
  Best Local Similarity   87.5%;  Pred. No. 53;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          3 WTLQDTCE 10
```

```
RESULT 7
ABR38932
ID   ABR38932 standard; protein; 15 AA.
XX
AC   ABR38932;
XX
DT   10-MAY-2003  (first entry)
XX
DE   HPV-11 E2 transactivation domain peptide fragment # SEQ ID 12.
XX
KW   Transactivation domain; HPV-11; E2 protein; TAD-inhibitor complex;
KW   binding.
XX
OS   Human papillomavirus.
XX
PN   WO2003006495-A2.
XX
PD   23-JAN-2003.
XX
PF   12-JUL-2002; 2002WO-CA001058.
XX
PR   12-JUL-2001; 2001US-0304412P.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (WANG/) WANG Y.
XX
PI   Cameron DR,  Archambault J,  Yoakim C,  White P;
XX
DR   WPI; 2003-239235/23.
XX
PT   Crystallizable composition comprising papilloma virus E2 transactivation
PT   domain-like polypeptide, complexed with an inhibitor, useful for
PT   providing information about inhibitor-binding pocket of transactivation
PT   domain.
XX
PS   Disclosure; Fig 10; 83pp; English.
XX
CC   The invention relates to a crystallizable composition, comprising a
CC   papilloma virus (PV) E2 transactivation domain (TAD)-like polypeptide
CC   complexed with an inhibitor. Compositions of the invention are useful for
CC   providing useful information on the inhibitor-binding pocket of the
CC   transactivation domain of the HPV-E2 protein. The HPV E2 TAD-inhibitor
CC   crystal structure can be used to identify the residues which are members
CC   of the HPV inhibitor binding pocket and which differ in the CRPV protein.
CC   The current sequence represents the HPV-11 E2 transactivation domain
CC   inhibitor-binding pocket peptide
XX
SQ   Sequence 15 AA;

  Query Match             36.7%;  Score 36;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||
Db          3 WTLQDT 8
```

```
RESULT 24
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ID   ADT50360 standard; peptide; 12 AA.
XX
AC   ADT50360;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Human non-muscular type myosin heavy-chain type A peptide Seq 14.
XX
KW   antigen; tumour; cancer; cytoskeletal; myosin;
KW   non-muscular type myosin heavy-chain type A; cytostatic; nmMHC.
XX
OS   Homo sapiens.
XX
PN   WO2004089984-A1.
XX
PD   21-OCT-2004.
XX
PF   03-OCT-2003; 2003WO-JP012732.
XX
PR   04-OCT-2002; 2002JP-00291953.
XX
PA   (MITS-) MITSUBISHI PHARMA CORP.
XX
PI   Hirakawa Y,  Niki H,  Oike S,  Tagawa T,  Hosokawa S,  Yoshiyama Y;
XX
DR   WPI; 2004-757952/74.
XX
PT   New non-muscular type myosin heavy chain type A antigen expressed on cell
PT   surface of tumor mass, useful as target in treatment of cancer such as
PT   stomach cancer.
XX
PS   Example 1; SEQ ID NO 14; 60pp; Japanese.
XX
CC   This invention relates to a novel antigen expressed on the surface of a
CC   cell during formation of a tumour mass. Specifically, it refers to a
CC   labelled ligand that is capable of recognising this antigen and a
CC   pharmaceutical composition derived thereof useful for treating a cancer
CC   patient. The present invention describes the antigen as a cytoskeletal
CC   protein such as myosin or its variant and preferably it is a non-muscular
CC   type myosin heavy-chain type A protein. Accordingly, the pharmaceutical
CC   compositions developed thereof exhibit cytostatic activity and are useful
CC   as anticancer agents in patients expressing this antigen and where the
CC   cancer is chosen from stomach, breast, colon or oesophageal cancer.
CC   Furthermore, the ligand is a monoclonal antibody, preferably a humanised
CC   monoclonal antibody that has cancer reactive properties and as such can
CC   specifically target the cancerous tissue or cell. This peptide sequence
CC   is derived from the human non-muscular type myosin heavy-chain (nmMHC)
CC   type A protein (the antigen), given in an exemplification of the
CC   invention.
XX
SQ   Sequence 12 AA;

  Query Match             32.7%;  Score 32;  DB 8;  Length 12;
  Best Local Similarity   85.7%;  Pred. No. 3.8e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 LQDTQEI 13
              |||||| :
Db          6 LQDTQEL 12
```

```
RESULT 2
US-09-641-528B-48934
; Sequence 48934, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48934
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-48934

  Query Match             38.8%;  Score 38;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 5e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          1 WTLQDTCE 8
```

```
RESULT 3
US-09-641-528B-50061
; Sequence 50061, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50061
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50061

  Query Match             38.8%;  Score 38;  DB 3;  Length 9;
  Best Local Similarity   87.5%;  Pred. No. 5e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          1 WTLQDTCE 8
```

```
RESULT 4
US-09-641-528B-3817
; Sequence 3817, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3817
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-3817

  Query Match             38.8%;  Score 38;  DB 3;  Length 10;
  Best Local Similarity   87.5%;  Pred. No. 7.4;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          1 WTLQDTCE 8
```

RESULT 5
US-09-641-528B-7824
; Sequence 7824, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10

```
RESULT 22
US-09-641-528B-3714
; Sequence 3714, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3714
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-3714

  Query Match             36.7%;  Score 36;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WTLQDT 10
              ||||||
Db          5 WTLQDT 10
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```
RESULT 25
US-09-641-528B-50612
; Sequence 50612, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
;  APPLICANT: Sette, Alessandro
;  APPLICANT:  Sidney, John
;  APPLICANT:  Southwood, Scott
;  APPLICANT:  Chesnut, Robert
;  APPLICANT:  Celis, Esteban
;  APPLICANT:  Grey, Howard
;  TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
;  TITLE OF INVENTION:  USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
;  FILE REFERENCE: 2060.0100001
;  CURRENT APPLICATION NUMBER: US/09/641,528B
;  CURRENT FILING DATE:  2000-08-15
;  PRIOR APPLICATION NUMBER: US 60/172,705
;  PRIOR FILING DATE: 1999-12-10
;  NUMBER OF SEQ ID NOS: 51505
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50612
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50612

  Query Match             36.7%;  Score 36;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WTLQDT 10
              ||||||
Db          9 WTLQDT 14
```

```
RESULT 1
US-10-715-810-95
; Sequence 95, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 95
;   LENGTH: 19
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 976-994)
US-10-715-810-95

  Query Match             75.5%;  Score 74;  DB 5;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GEIIWTLQDTQEIK 14
              ||||||||||||||
Db          6 GEIIWTLQDTQEIK 19
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```
RESULT 3
US-10-193-460A-22
; Sequence 22, Application US/10193460A
; Publication No. US20030082769A1
; GENERAL INFORMATION:
;  APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
;  TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS E2 TRANSACTIVATION
;  TITLE OF INVENTION:  DOMAIN/INHIBITOR CO-CRYSTAL AND X-RAY COORDINATES DEFINING
;  TITLE OF INVENTION:  THE INHIBITOR-BINDING POCKET
;  FILE REFERENCE: 13/100
;  CURRENT APPLICATION NUMBER: US/10/193,460A
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: 60/304,412
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: HPV18
US-10-193-460A-22

  Query Match             38.8%;  Score 38;  DB 4;  Length 15;
  Best Local Similarity   87.5%;  Pred. No. 39;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 WTLQDTQE 12
              |||||| |
Db          3 WTLQDTCE 10
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RESULT 5
US-10-193-460A-12
; Sequence 12, Application US/10193460A
; Publication No. US20030082769A1
; GENERAL INFORMATION:
;  APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
;  TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS E2 TRANSACTIVATION
;  TITLE OF INVENTION:  DOMAIN/INHIBITOR CO-CRYSTAL AND X-RAY COORDINATES DEFINING
;  TITLE OF INVENTION:  THE INHIBITOR-BINDING POCKET
;  FILE REFERENCE: 13/100
;  CURRENT APPLICATION NUMBER: US/10/193,460A
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: 60/304,412
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: HPV11
US-10-193-460A-12

  Query Match             36.7%;  Score 36;  DB 4;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WTLQDT 10
              ||||||
Db          3 WTLQDT 8
```

```
RESULT 19
US-10-530-171-14
; Sequence 14, Application US/10530171
; Publication No. US20060057147A1
; GENERAL INFORMATION:
;  APPLICANT: HIRAKAWA, Youko
;  APPLICANT:  NIKI, Hisae
;  APPLICANT:  OIKE, Shinsuke
;  APPLICANT:  TAGAWA, Toshiaki
;  APPLICANT:  HOSOKAWA,Saiko
;  APPLICANT:  YOSHIYAMA, Yoshiko
;  TITLE OF INVENTION: Antibody recognizing antigen
;  FILE REFERENCE: 235054
;  CURRENT APPLICATION NUMBER: US/10/530,171
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/JP2003/012732
;  PRIOR FILING DATE: 2003-10-03
;  PRIOR APPLICATION NUMBER: JP 2002-291953
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-530-171-14

  Query Match             32.7%;  Score 32;  DB 5;  Length 12;
  Best Local Similarity   85.7%;  Pred. No. 2.9e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 LQDTQEI 13
              ||||||:
Db          6 LQDTQEL 12
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DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 13-OCT-1994 (first entry)
XX
DE Rat HCNP precursor internal fragment #9.
XX
KW Rat hippocampal cholinergic neurotrophic peptide; rat HCNP;
KW nerve degeneration; acetylcholine synthesis; neurostimulation.
XX
OS Rattus norvegicus; (Wistar).
XX
PN WO9405788-A1.
XX
PD 17-MAR-1994.
XX
PF 27-AUG-1993; 93WO-JP001214.
XX
PR 28-AUG-1992; 92JP-00254170.
PR 29-AUG-1992; 92JP-00253734.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (YAMA/) YAMAMOTO M.
XX
PI Ojika K, Tohdoh N, Tojo S, Kojima S, Fukushima N, Irie T, Ono K;
PI Agui H, Ueki Y, Nishihara T, Kamikawa Y, Taiji M;
XX
DR WPI; 1994-101193/12.
XX
PT Neurotrophic peptide(s), precursors and genes - used to treat nervous
PT degeneration, increases acetylcholine synthesis.
XX
PS Example 9; Page 161; 200pp; Japanese.
XX
CC The rat hippocampal cholinergic neurotrophic peptide precursor was
CC digested by lysyl endopeptidase and the resultant peptide fragments were
CC sequenced. Peptide AAR49954 is an internal fragment. (Updated on 25-MAR-
CC 2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 28 AA;

Query Match 32.1%; Score 36; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy         14 HRYIWI 19
                |||:|:
Db          5 HRYVWL 10
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RESULT 6
US-08-403-378B-10
; Sequence 10, Application US/08403378B
; Patent No. 5759991
;  GENERAL INFORMATION:
;    APPLICANT:  TOHDOH, NAOKI
;    APPLICANT:  TOJO, SHIN-ICHIRO
;    APPLICANT:  KOJIMA, SHIN-ICHI
;    APPLICANT:  UEKI, YASUYUKI
;    APPLICANT:  NISHIHARA, TOSHIO
;    APPLICANT:  FUKUSHIMA, NOBUYUKI
;    APPLICANT:  IRIE, TSUNEMASA
;    APPLICANT:  ONO, KEIICHI
;    APPLICANT:  AGUI, HIDEO
;    APPLICANT:  OJIKA, KOSEI
;    TITLE OF INVENTION:  NEUROTROPHIC PEPTIDE DERIVATIVES
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 PENNSYLVANIA AVENUE, NW
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/403,378B
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-124688
;      FILING DATE:  27-APR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-080398
;      FILING DATE:  30-MAR-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-280590
;      FILING DATE:  27-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 1-333241
;      FILING DATE:  21-DEC-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 2-243003
;      FILING DATE:  12-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/758,043
;      FILING DATE:  12-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/873,764
;      FILING DATE:  27-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/01214
;      FILING DATE:  27-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BIGGART, WADDELL A
;      REGISTRATION NUMBER:  24,861
;      REFERENCE/DOCKET NUMBER:
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  28 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  rattus norvegicus
;      STRAIN:  Wistar
;      TISSUE TYPE:  hippocampal tissue of brain
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..28
US-08-403-378B-10

  Query Match             32.1%;  Score 36;  DB 1;  Length 28;
  Best Local Similarity   66.7%;  Pred. No. 46;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 HRYIWI 19
              |||:|:
Db          5 HRYVWL 10
```

```
RESULT 28
US-10-776-521B-280
; Sequence 280, Application US/10776521B
; Publication No. US20050202033A1
; GENERAL INFORMATION:
;  APPLICANT: Fletchner, Jessica
;  APPLICANT:  Prince-Cohane, Kenya
;  APPLICANT:  Mehta, Sunil
;  APPLICANT:  Slusarewicz, Paul
;  APPLICANT:  Andjelic, Sofija
;  APPLICANT:  Barber, Brian
;  TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
;  TITLE OF INVENTION:  IMMUNOTHERAPIES
;  FILE REFERENCE: 8449-405-999
;  CURRENT APPLICATION NUMBER: US/10/776,521B
;  CURRENT FILING DATE:  2004-02-12
;  PRIOR APPLICATION NUMBER: 60/503,417
;  PRIOR FILING DATE: 2003-09-16
;  PRIOR APPLICATION NUMBER: 60/463,746
;  PRIOR FILING DATE: 2003-04-18
;  PRIOR APPLICATION NUMBER: 60/462,469
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/447,142
;  PRIOR FILING DATE: 2003-02-13
;  NUMBER OF SEQ ID NOS: 419
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 280
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Heat shock protein binding domain with a terminal
;   OTHER INFORMATION: Trp residue
US-10-776-521B-280

  Query Match             29.5%;  Score 33;  DB 5;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1.9e+06;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 THRYIW 18
              |||::|
Db          3 THRWLW 8
```

```
GenCore version 5.1.9
                  Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          November  1, 2006, 12:29:25 ; Search time 84.8 Seconds
                                            (without alignments)
                                            102.442 Million cell updates/sec

Title:           US-10-821-669-1_COPY_1051_1069
Perfect score:   112
Sequence:        1 NNIMFKLDGCRDTHRYIWI 19

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1000 summaries

Database :        A_Geneseq_8:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*
                 9:  geneseqp2005s:*
                 10:  geneseqp2006s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES

                  %
Result            Query
   No.    Score  Match Length DB  ID                          Description
 ----------------------------------------------------------------------------
     1      112  100.0     19  9  ADW11084                    Adw11084 Clostridi
```

```
RESULT 4
A25310
alpha-amylase/trypsin inhibitor CM1 - wheat (fragment)
C;Species: Triticum aestivum (common wheat)
C;Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 31-Dec-2004
C;Accession: A25310
R;Barber, D.; Sanchez-Monge, R.; Garcia-Olmedo, F.; Salcedo, G.; Mendez, E.
Biochim. Biophys. Acta 873, 147-151, 1986
A;Title: Evolutionary implications of sequential homologies among members of the tryps
A;Reference number: A90661
A;Accession: A25310
A;Molecule type: protein
A;Residues: 1-28
A;Cross-references: UNIPROT:P16850; UNIPARC:UPI00001763DE
A;Experimental source: cv. Candeal
C;Superfamily: alpha-amylase/trypsin inhibitor
C;Keywords: alpha-amylase inhibitor

  Query Match             25.0%;  Score 28;  DB 2;  Length 28;
  Best Local Similarity   66.7%;  Pred. No. 7.2e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 LDGCRD 12
              |:|||:
Db         16 LEGCRE 21
```

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RESULT 49
Q57YV8_HUMAN
ID   Q57YV8_HUMAN   PRELIMINARY;   PRT;    17 AA.
AC   Q57YV8;
DT   10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   10-MAY-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Hypothetical protein TPO (Fragment).
GN   Name=TPO;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.H.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Wilson R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Wilson R.K.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AC141930; AAX82037.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   17 AA;  1896 MW;  51C4B9D9295ACAB2 CRC64;

  Query Match             25.9%;  Score 29;  DB 2;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 RDTHR 15
              |||||
Db          8 RDTHR 12
```

```
RESULT 26
ADR46808
ID   ADR46808 standard; peptide; 21 AA.
XX
AC   ADR46808;
XX
DT   04-NOV-2004  (first entry)
XX
DE   H. influenzae hap protein conserved peptide #33.
XX
KW   immunostimulant; antibacterial; vaccine; adhesion; penetration;
KW   immunogenic; Haemophilus infection; hap.
XX
OS   Haemophilus influenzae.
XX
PN   US2004157241-A1.
XX
PD   12-AUG-2004.
XX
PF   15-OCT-2003; 2003US-00687046.
XX
PR   25-AUG-1994;   94US-00296791.
PR   20-APR-2001; 2001US-00839996.
PR   22-FEB-2002; 2002US-00080505.
XX
PA   (SGEM/) ST GEME J W.
XX
PI   St Geme JW;
XX
DR   WPI; 2004-592770/57.
XX
PT   New Haemophilus adhesion and penetration protein, useful for inducing an
PT   immune response against Haemophilus infection and for treating and
PT   preventing Haemophilus infection.
XX
PS   Disclosure; SEQ ID NO 50; 144pp; English.
XX
CC   The invention relates to a recombinant Haemophilus adhesion and
CC   penetration protein. The recombinant Haemophilus adhesion and penetration
CC   protein, nucleic acid, methods, composition, antibodies and vaccines are
CC   useful for inducing an immune response against Haemophilus infection and
CC   for treating and preventing Haemophilus infection. The present sequence
CC   represents the amino acid sequence of an H. influenzae hap protein
CC   conserved peptide.
XX
SQ   Sequence 21 AA;

  Query Match             30.8%;  Score 32;  DB 8;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. 6.2e+02;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YVDVNNVGIR 11
              ||||:|  ::
Db          8 YVDVSNANVQ 17
```

```
RESULT 6
US-10-080-505-50
; Sequence 50, Application US/10080505
; Patent No. 6676948
; GENERAL INFORMATION:
;  APPLICANT: St. Geme, Joseph W.
;  TITLE OF INVENTION: HAEMOPHILUS ADHERENCE AND PENETRATION PROTIENS
;  FILE REFERENCE: A-59941-1/RFT/DCF/DHR
;  CURRENT APPLICATION NUMBER: US/10/080,505
;  CURRENT FILING DATE:  2002-02-22
;  PRIOR APPLICATION NUMBER: US 08/296,791
;  PRIOR FILING DATE: 1994-10-25
;  PRIOR APPLICATION NUMBER: US 09/839,996
;  PRIOR FILING DATE: 2001-04-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Haemophilus influenzae
US-10-080-505-50

  Query Match             30.8%;  Score 32;  DB 2;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YVDVNNVGIR 11
              ||||:|  ::
Db          8 YVDVSNANVQ 17
```

```
RESULT 22
US-09-068-804-28
; Sequence 28, Application US/09068804
; Patent No. 6861247
;  GENERAL INFORMATION:
;    APPLICANT:  Miller, Samuel I.
;    TITLE OF INVENTION:  SALMONELLA SECRETED PROTEINS
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/068,804
;      FILING DATE:  14-MAY-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/18504
;      FILING DATE:  14-NOV-1996
;      APPLICATION NUMBER:  60/006,733
;      FILING DATE:  14-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00786/292002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-068-804-28

  Query Match             28.8%;  Score 30;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 VNNVGIRGYMYL 16
              ::||||    ||
Db          3 ISNVGINPAAYL 14
```

```
RESULT 23
US-09-068-804-30
; Sequence 30, Application US/09068804
; Patent No. 6861247
;  GENERAL INFORMATION:
;    APPLICANT:  Miller, Samuel I.
;    TITLE OF INVENTION:  SALMONELLA SECRETED PROTEINS
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/068,804
;      FILING DATE:  14-MAY-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/18504
;      FILING DATE:  14-NOV-1996
;      APPLICATION NUMBER:  60/006,733
;      FILING DATE:  14-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fraser, Janis K.
;      REGISTRATION NUMBER:  34,819
;      REFERENCE/DOCKET NUMBER:  00786/292002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-068-804-30

  Query Match             28.8%;  Score 30;  DB 2;  Length 15;
  Best Local Similarity   50.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 VNNVGIRGYMYL 16
              ::||||    ||
Db          3 ISNVGINPAAYL 14
```

```
 Sequence 59, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
;  APPLICANT: Neben, Steven
;  APPLICANT:  Takeuchi, Toshihiko
;  APPLICANT:  Tomkinson, Adrian
;  TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
;  TITLE OF INVENTION:  Treatment Of Asthma
;  FILE REFERENCE: 7430*163
;  CURRENT APPLICATION NUMBER: US/10/320,231A
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/342,174
;  PRIOR FILING DATE: 2001-12-17
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic sequence
US-10-320-231A-59

  Query Match             28.8%;  Score 30;  DB 4;  Length 11;
  Best Local Similarity   83.3%;  Pred. No. 5.8e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GIRGYM 14
              |||||:
Db          5 GIRGYL 10
```

```
Sequence 506, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
;  APPLICANT: EDWARDS, ALED
;  APPLICANT:  DHARAMSI, AKIL
;  APPLICANT:  VEDADI, MASOUD
;  TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
;  FILE REFERENCE: IPT-330.01
;  CURRENT APPLICATION NUMBER: US/11/122,986
;  CURRENT FILING DATE:  2005-05-05
;  PRIOR APPLICATION NUMBER: 60/423,875
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,832
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,915
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,757
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,758
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/424,367
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,376
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,370
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,362
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,373
;  PRIOR FILING DATE: 2002-11-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 844
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 506
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-11-122-986-506

  Query Match             26.0%;  Score 27;  DB 7;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 MYLKGP 19
               :||:||
Db           2 LYLQGP 7
```

```
 Sequence 353, Application US/11313152
; Publication No. US20060153858A1
; GENERAL INFORMATION:
;  APPLICANT: Kundig, Thomas M.
;  APPLICANT:  Simard, John J. L.
;  TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE
;  FILE REFERENCE: MANNK.001CP2C1
;  CURRENT APPLICATION NUMBER: US/11/313,152
;  CURRENT FILING DATE:  2005-12-19
;  PRIOR APPLICATION NUMBER: 09/776,232
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 09/380,534
;  PRIOR FILING DATE: 1999-09-01
;  PRIOR APPLICATION NUMBER: PCT/US98/14289
;  PRIOR FILING DATE: 1998-07-10
;  PRIOR APPLICATION NUMBER: 08/988,320
;  PRIOR FILING DATE: 1997-12-10
;  PRIOR APPLICATION NUMBER: CA 2,209,815
;  PRIOR FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 569
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 353
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Haemophilus influenzae
US-11-313-152-353

  Query Match             25.0%;  Score 26;  DB 7;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 RGYMY 15
               |||:|
Db           1 RGYVY 5
```

```
RESULT 48
US-11-409-939-38
; Sequence 38, Application US/11409939
; Publication No. US20060240018A1
;   GENERAL INFORMATION:
;        APPLICANT: Koieda, Shohei
;        TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
;        NUMBER OF SEQUENCES: 118
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
;             STREET: 121 South Eighth Street, Ste. 1600
;             CITY: Minneapolis
;             STATE: MN
;             COUNTRY: USA
;             ZIP: 55402
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/409,939
;             FILING DATE: 24-Apr-2006
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/096,749
;             FILING DATE: June 12, 1998
;             APPLICATION NUMBER:
;             FILING DATE:
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ann S. Viksnins
;             REGISTRATION NUMBER: 37,748
;             REFERENCE/DOCKET NUMBER: 109.034US1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (612) 373-6900
;             TELEFAX: (612) 339-3061
;   INFORMATION FOR SEQ ID NO: 38:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 7 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        FRAGMENT TYPE: internal
;        ORIGINAL SOURCE:
;        SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-11-409-939-38

  Query Match             24.0%;  Score 25;  DB 7;  Length 7;
  Best Local Similarity   66.7%;  Pred. No. 3e+05;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 RGYMYL 16
               ||:|:|
Db           1 RGFMWL 6
```

```
RESULT 4
B85928
hypothetical protein Z4088 [imported] - Escherichia coli (strain O157:H7, substrain ED
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85928
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85928
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25
A;Cross-references: UNIPROT:Q8X3V1; UNIPARC:UPI00000D0EA3; GB:AE005174; NID:g12517242;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4088

  Query Match             26.0%;  Score 27;  DB 2;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 6.8e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GIRGYM 14
              |:|||:
Db         14 GLRGYV 19
```

```
RESULT 4
Q6R273_LACLC
ID   Q6R273_LACLC   PRELIMINARY;   PRT;    12 AA.
AC   Q6R273;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   ArgC (Fragment).
GN   Name=argC;
OS   Lactococcus lactis subsp. cremoris (Streptococcus cremoris).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX   NCBI_TaxID=1359;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MG1363;
RX   PubMed=14762010; DOI=10.1128/JB.186.4.1147-1157.2004;
RA   Larsen R., Buist G., Kuipers O.P., Kok J.;
RT   "ArgR and AhrC are both required for regulation of arginine metabolism
RT   in Lactococcus lactis.";
RL   J. Bacteriol. 186:1147-1157(2004).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY518514; AAR99645.1; -; Genomic_DNA.
FT   NON_TER      12      12
SQ   SEQUENCE   12 AA;  1335 MW;  CC8E9BF86162C05D CRC64;

  Query Match             30.8%;  Score 32;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 VGIRGY 13
              ||||||
Db          7 VGIRGY 12
```

```
RESULT 6
Q9GLI9_PIG
ID   Q9GLI9_PIG     PRELIMINARY;   PRT;    21 AA.
AC   Q9GLI9;
DT   01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2001, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Leucine aminopeptidase (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Smith T.P.L., Fahrenkrug S.C., Rohrer G.A., Simmen F.A.,
RA   Rexroad C.E. III, Keele J.W.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF267719; AAG25934.1; -; Genomic_DNA.
DR   HSSP; P00727; 1LAM.
DR   MEROPS; M17.005; -.
DR   GO; GO:0004177; F:aminopeptidase activity; IEA.
KW   Aminopeptidase.
FT   NON_TER       1      1
FT   NON_TER      21     21
SQ   SEQUENCE   21 AA;  2198 MW;  7C2EF81999015E1F CRC64;

  Query Match             29.8%;  Score 31;  DB 2;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.4e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DVNNVG 9
              ||||:|
Db          7 DVNNIG 12
```

```
RESULT 42
Q8X3V1_ECO57
ID   Q8X3V1_ECO57   PRELIMINARY;   PRT;    25 AA.
AC   Q8X3V1;
DT   01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2002, sequence version 1.
DT   07-FEB-2006, entry version 13.
DE   No significant matches.
GN   OrderedLocusNames=z4088;
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX   MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
CC   -----------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----------------------------------------------------------------------
DR   EMBL; AE005174; AAG57886.1; -; Genomic_DNA.
DR   PIR; B85928; B85928.
KW   Complete proteome.
SQ   SEQUENCE   25 AA;  3152 MW;  0C2F84A4E0257B77 CRC64;

  Query Match             26.0%;  Score 27;  DB 2;  Length 25;
  Best Local Similarity   66.7%;  Pred. No. 7.9e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GIRGYM 14
              |:|||:
Db         14 GLRGYV 19
```

RESULT 23
ABO12635
ID ABO12635 standard; peptide; 25 AA.
XX
AC ABO12635;
XX
DT 25-AUG-2003 (first entry)
XX
DE Human zinc finger DNA binding domain #934.
XX
KW Composite binding polypeptide; zinc finger nucleic acid binding domain;
KW autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;
KW human.
XX
OS Homo sapiens.
XX
PN WO200299084-A2.
XX
PD 12-DEC-2002.
XX
PF 04-APR-2002; 2002WO-US022272.
XX
PR 04-APR-2001; 2001GB-00008491.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Moore M, Sepp A, Isalan M, Choo Y;
XX
DR WPI; 2003-278214/27.
XX
PT New composite binding zinc finger polypeptide, useful for designing
PT sequence-specific binding proteins regulating gene expression in the
PT fields of molecular biology, and for the diagnosis and treatment of
PT autoimmune disorders.
XX
PS Example 2; Page 91; 157pp; English.
XX
CC The invention relates to a composite binding polypeptide comprising a
CC first natural binding domain derived from a first natural binding
CC polypeptide and a second natural binding domain derived from a second
CC natural binding polypeptide, where the first and second natural binding
CC polypeptides may be the same or different and where the polypeptide binds
CC to a target differing from the natural target of both the first and
CC second binding polypeptides. The invention also relates to a chimeric
CC polypeptide comprising a binding polypeptide cited above and a biological
CC effector domain, a library of natural binding domains, a library of
CC natural zinc finger nucleic acid binding domains comprising a linker
CC attached to it, a method for selecting a binding polypeptide capable of
CC binding to a target site and a method for designing a composite binding
CC polypeptide. The methods and compositions of the present invention are
CC useful for designing sequence-specific binding proteins for regulation of
CC gene expression in the fields of molecular biology. They can also be used
CC for the diagnosis and treatment of autoimmune disorders, and as research
CC tools and in transgenic animals. This sequence represents a human zinc
CC finger DNA binding domain used in the scope of the invention
XX
SQ Sequence 25 AA;

  Query Match   30.8%; Score 40; DB 6; Length 25;
  Best Local Similarity   54.5%; Pred. No. 1.6e+02;
  Matches   6; Conservative   2; Mismatches   3; Indels   0; Gaps   0;

```
Qy          5 GCSWEFIPVDD 15
              ||||:|   |:
Db          7 GCSWKFARSDE 17
```

RESULT 1
US-[redacted]
; Sequence 105, Application US[redacted]
; Publication No. US20050106182A1
; GENERAL INFORMATION:
; APPLICANT: Li, Shengwen
; APPLICANT: Kei, Aoki R.
; TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
; FILE REFERENCE: ALLE0004-100
; CURRENT APPLICATION NUMBER: US[redacted]
; CURRENT FILING DATE: 2003-11-17
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragment (residues 1277-1296)
US-10-715-810-105

1275-1296

Query Match 93.1%; Score 121; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 TLGCSWEFIPVDDGWGERPL 22
              ||||||||||||||||||||
Db          1 TLGCSWEFIPVDDGWGERPL 20
```

```
RESULT 37
US-10-732-620-9
; Sequence 9, Application US/10732620
; Publication No. US20050032186A1
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jin-Soo
;  APPLICANT:  Shin, Hyun-Chul
;  APPLICANT:  Kwon, Heung-Sun
;  TITLE OF INVENTION: REGULATORY ZINC FINGER PROTEINS
;  FILE REFERENCE: 12279-009001
;  CURRENT APPLICATION NUMBER: US/10/732,620
;  CURRENT FILING DATE:  2003-12-09
;  PRIOR APPLICATION NUMBER: US 60/431,892
;  PRIOR FILING DATE: 2002-12-09
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 25
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-732-620-9

  Query Match             28.5%;  Score 37;  DB 5;  Length 25;
  Best Local Similarity   45.5%;  Pred. No. 5.2e+02;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCSWEFIPVDD 15
              ||:|:|   |:
Db          7 GCTWKFARSDE 17


RESULT 38
```

```
Sequence 92, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
;  APPLICANT: Parekh, Rajesh
;  TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
;  TITLE OF INVENTION:  SCHIZOPHRENIA
;  FILE REFERENCE: 9195-061-999
;  CURRENT APPLICATION NUMBER: US/09/791,378
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/750,395
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 677
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-378-92

  Query Match             27.7%;  Score 36;  DB 3;  Length 14;
  Best Local Similarity   66.7%;  Pred. No. 4.1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 IPVDDGWGE 19
              ||::|| ||
Db          1 IPIEDGSGE 9
```

ADV55232
ID ADV55232 standard; peptide; 14 AA.
XX
AC ADV55232;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 2729.
XX
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZW.
PA (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 2729; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
SQ Sequence 14 AA;

```
  Query Match             37.4%;  Score 37;  DB 9;  Length 14;
  Best Local Similarity   66.7%;  Pred. No. 68;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EENISLDLI 9
              |||::|||:
Db          4 EENVTLDLV 12
```

```
RESULT 19
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental aller
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11
A;Cross-references: UNIPARC:UPI000017C9F3
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

  Query Match             24.2%;  Score 24;  DB 2;  Length 11;
  Best Local Similarity   57.1%;  Pred. No. 8.1e+02;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 SLDLIQQ 11
              |:||::|
Db          5 SMDLMEQ 11
```

```
RESULT 20
S41601
interferon alpha receptor 1 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 25-Dec-1994 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
C;Accession: S41601
R;Abramovich, C.; Ratovitski, E.; Lundgren, E.; Revel, M.
FEBS Lett. 338, 295-300, 1994
A;Title: Identification of mRNAs encoding two different soluble forms of the human int
A;Reference number: S41601; MUID:94139943; PMID:8307198
A;Accession: S41601
A;Molecule type: mRNA
A;Residues: 1-14
A;Cross-references: UNIPARC:UPI000017C27A
C;Keywords: cytokine receptor

  Query Match             24.2%;  Score 24;  DB 2;  Length 14;
  Best Local Similarity   83.3%;  Pred. No. 1.1e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 ENISLD 7
              |||||:
Db          7 ENISLN 12
```

```
RESULT 43
S38527
rRNA N-glycosidase (EC 3.2.2.22) saporin S6 - common soapwort (fragment)
C;Species: Saponaria officinalis (common soapwort)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 02-Jul-1998
C;Accession: S38527
R;Ferreras, J.M.; Barbieri, L.; Girbes, T.; Battelli, M.G.; Rojo, M.A.; Arias, F.J.; R
Biochim. Biophys. Acta 1216, 31-42, 1993
A;Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRN
A;Reference number: S38521; MUID:94032486; PMID:8218413
A;Accession: S38527
A;Molecule type: protein
A;Residues: 1-30
A;Cross-references: UNIPARC:UPI0000174670
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: glycosidase; hydrolase

  Query Match             23.2%;  Score 23;  DB 2;  Length 30;
  Best Local Similarity   57.1%;  Pred. No. 3.5e+03;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 NISLDLI 9
              :|:|||:
Db          3 SITLDLV 9
```

```
B61497
seed protein ws-17 - winged bean (fragment)
C;Species: Psophocarpus tetragonolobus (winged bean)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: B61497
R;Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-d
A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: B61497
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12
A;Cross-references: UNIPROT:Q7M1H9; UNIPARC:UPI000017B06B
C;Keywords: seed

  Query Match             22.2%;  Score 22;  DB 2;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 LTFNFD 19
              ::|||:
Db          3 ISFNFN 8
```

```
PA0007
lectin B1 - Psophocarpus scandens (fragment)
C;Species: Psophocarpus scandens
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: PA0007
R;Kortt, A.A.
Phytochemistry 27, 2847-2855, 1988
A;Title: Isolation and characterization of the lectins from the seeds of Psophocarpus
A;Reference number: PA0005
A;Accession: PA0007
A;Molecule type: protein
A;Residues: 1-14
A;Cross-references: UNIPROT:P22584; UNIPARC:UPI000012E3DA
A;Experimental source: seed
C;Comment: The seeds of Psophocarpus contain two distinct groups of lectins which can
C;Keywords: lectin

  Query Match             22.2%;  Score 22;  DB 2;  Length 14;
  Best Local Similarity   50.0%;  Pred. No. 2.2e+03;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 LTFNFD 19
              ::|||:
Db          3 ISFNFN 8
```

```
 Sequence 225, Application US/10666480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
;  APPLICANT: Boone, Thomas C
;  APPLICANT:  Wild, Kenneth D
;  APPLICANT:  Sitney, Karen C
;  APPLICANT:  Min, Hosung
;  APPLICANT:  Kimmel, Bruce
;  TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Facto
;  FILE REFERENCE: A-827US
;  CURRENT APPLICATION NUMBER: US/10/666,480
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: 60/412,524
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 286
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Therapeutically active peptide of randomly generated,  non-natu
;   OTHER INFORMATION: lly occurring sequence
US-10-666-480-225

  Query Match             31.3%;  Score 31;  DB 4;  Length 26;
  Best Local Similarity   55.6%;  Pred. No. 1.6e+03;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 SLDLIQQYY 13
              || |::||:
Db          9 SLPLVEQYF 17
```

```
Sequence 178, Application US/10948707
; Publication No. US20050187147A1
; GENERAL INFORMATION:
;  APPLICANT: Ballatore, Carlo
;  APPLICANT:  Castellino, Angelo
;  APPLICANT:  Desharnais, Joel
;  APPLICANT:  Guo, Zijian
;  APPLICANT:  Li, Qing
;  APPLICANT:  Newman, Michael James
;  APPLICANT:  Sun, Chengzao
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
;  TITLE OF INVENTION:  DRUG EFFICIENCY
;  FILE REFERENCE: 17967-003001
;  CURRENT APPLICATION NUMBER: US/10/948,707
;  CURRENT FILING DATE:  2004-09-22
;  PRIOR APPLICATION NUMBER: 60/505,325
;  PRIOR FILING DATE: 2003-09-22
;  PRIOR APPLICATION NUMBER: 60/568,340
;  PRIOR FILING DATE: 2004-05-04
;  PRIOR APPLICATION NUMBER: 60/581,835
;  PRIOR FILING DATE: 2004-06-22
;  NUMBER OF SEQ ID NOS: 1422
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 178
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-948-707-178

  Query Match             30.3%;  Score 30;  DB 5;  Length 9;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+06;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EENISLD 7
              |||:|:|
Db          1 EENVSVD 7
```

```
Sequence 225, Application US/10666480
; Patent No. 6919426
; GENERAL INFORMATION:
;  APPLICANT: Boone, Thomas C
;  APPLICANT:  Wild, Kenneth D
;  APPLICANT:  Sitney, Karen C
;  APPLICANT:  Min, Hosung
;  APPLICANT:  Kimmel, Bruce
;  TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Facto
;  FILE REFERENCE: A-827US
;  CURRENT APPLICATION NUMBER: US/10/666,480
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: 60/412,524
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 286
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Therapeutically active peptide of randomly generated,  non-natu
;   OTHER INFORMATION: lly occurring sequence
US-10-666-480-225

  Query Match             31.3%;  Score 31;  DB 2;  Length 26;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 SLDLIQQYY 13
              || |::||:
Db          9 SLPLVEQYF 17
```

```
Sequence 57, Application US/08188583
; Patent No. 5851813
;  GENERAL INFORMATION:
;    APPLICANT:  Desrosiers, Ronald C.
;    TITLE OF INVENTION:  PRIMATE LENTIVIRUS VACCINES
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/188,583
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/727,494
;      FILING DATE:  July 9, 1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/551,945
;      FILING DATE:  July 12, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  Reg. No. 5851813 29,066
;      REFERENCE/DOCKET NUMBER:  00246/079002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-188-583-57

  Query Match             28.3%;  Score 28;  DB 1;  Length 13;
  Best Local Similarity   57.1%;  Pred. No. 2.9e+02;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 QQYYLTF 16
               :::||||
Db           3 EEHYLTF 9
```

SCORE Search Results Details for Application 10821669 and Search Result us-10-821-669-1_copy_519_537.szlm30.rag.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10821669 and Search Result us-10-821-669-1_copy_519_537.szlm30.rag.

start

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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_519_537
Perfect score: 94
Sequence: 1 NLSSDIIGQLELMPNIERF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94	100.0	19	9	ADW11046	Adw11046 Clostridi
2	94	100.0	27	9	ADW11104	Adw11104 Clostridi
3	47	50.0	27	9	ADW11105	Adw11105 Clostridi
4	38	40.4	24	2	AAR84289	Aar84289 Aq. elcat
5	37	39.4	30	2	AAR07952	Aar07952 Synthetic
6	34.5	36.7	30	6	ABP80164	Abp80164 N. gonorr
7	34	36.2	15	9	AEC39638	Aec39638 Bovine a-
8	33	35.1	16	3	AAB19666	Aab19666 Alkaloid
9	33	35.1	28	2	AAW54070	Aaw54070 IVI-4 pro
10	32	34.0	18	9	AEC79872	Aec79872 Human cDN
11	32	34.0	22	3	AAB21083	Aab21083 GDF-8 inh
12	32	34.0	25	5	ABG62351	Abg62351 Eubacteri
13	32	34.0	29	10	AEE37974	Aee37974 Human ser
14	31	33.0	10	8	ADQ26479	Adq26479 Post-tran
15	31	33.0	12	4	ABP17479	Abp17479 HIV B27 s
16	31	33.0	12	9	AEA47509	Aea47509 Amino aci
17	31	33.0	14	8	ADQ26478	Adq26478 Post-tran
18	31	33.0	14	9	AEA47508	Aea47508 Amino aci
19	31	33.0	14	9	AEA47503	Aea47503 Amino aci
20	31	33.0	14	9	AEA47511	Aea47511 Amino aci
21	31	33.0	14	9	AEA47510	Aea47510 Amino aci
22	31	33.0	14	9	AEA33936	Aea33936 Mass spec
23	31	33.0	14	9	AEC01306	Aec01306 Alpha-cas
24	31	33.0	14	9	AEC39624	Aec39624 Bovine a-
25	31	33.0	14	9	AEF22727	Aef22727 Alpha-cas
26	31	33.0	14	10	AEE60013	Aee60013 Alpha-S1-
27	31	33.0	16	9	AEC39625	Aec39625 Bovine a-
28	31	33.0	16	9	AEF22728	Aef22728 Alpha-cas
29	31	33.0	16	10	AEE60014	Aee60014 Alpha-S1-
30	31	33.0	16	10	AEE60011	Aee60011 Alpha-S1-
31	31	33.0	17	9	AEC39626	Aec39626 Bovine a-
32	31	33.0	17	9	AEF22729	Aef22729 Alpha-cas
33	31	33.0	19	5	AAE23255	Aae23255 Database
34	31	33.0	20	2	AAW11227	Aaw11227 Modified
35	31	33.0	20	9	AED19922	Aed19922 Canine pa
36	31	33.0	20	9	AEE34594	Aee34594 Wheat gli
37	31	33.0	21	5	AAU89641	Aau89641 Insulin/i
38	31	33.0	22	8	ADQ81655	Adq81655 E_faecali
39	31	33.0	23	2	AAW09056	Aaw09056 Epstein-B
40	31	33.0	23	4	AAB91905	Aab91905 Bombesin
41	31	33.0	30	4	ABB50580	Abb50580 Human sec
42	31	33.0	30	6	ABO44837	Abo44837 Novel hum
43	31	33.0	30	7	ABO26317	Abo26317 Protein a
44	30	31.9	7	2	AAR86583	Aar86583 Autotaxin
45	30	31.9	11	8	ADQ81646	Adq81646 E_faecali
46	30	31.9	12	2	AAR66882	Aar66882 Agonist p
47	30	31.9	12	2	AAW01915	Aaw01915 C140 rece
48	30	31.9	13	2	AAR66881	Aar66881 Agonist p
49	30	31.9	13	2	AAW01914	Aaw01914 C140 rece
50	30	31.9	14	2	AAW88297	Aaw88297 Human gua
51	30	31.9	15	8	ADN65558	Adn65558 HLA bindi
52	30	31.9	20	9	AEE34405	Aee34405 Wheat gli
53	30	31.9	20	9	AEE34587	Aee34587 Wheat gli
54	30	31.9	23	4	ABB43858	Abb43858 Peptide #
55	30	31.9	23	4	AAM37771	Aam37771 Peptide #
56	30	31.9	23	4	AAM64837	Aam64837 Human bra
57	30	31.9	23	4	ABG59233	Abg59233 Human liv

58	30	31.9	23	5	ABG46617	Abg46617 Human pep
59	30	31.9	24	2	AAR85557	Aar85557 Aqueous e
60	30	31.9	24	4	AAG99617	Aag99617 ERA bindi
61	30	31.9	25	2	AAR85556	Aar85556 Aqueous e
62	30	31.9	25	2	AAY33336	Aay33336 U. pugila
63	30	31.9	25	3	AAB22958	Aab22958 Fiddler c
64	30	31.9	25	3	AAY93927	Aay93927 N-termina
65	30	31.9	25	4	AAE07933	Aae07933 N-termina
66	30	31.9	25	5	ABG62547	Abg62547 Eubacteri
67	30	31.9	25	5	ABG62353	Abg62353 Eubacteri
68	30	31.9	25	5	AAO21350	Aao21350 Uca pugil
69	30	31.9	25	9	ADY81714	Ady81714 Krill-der
70	30	31.9	27	3	AAB44738	Aab44738 Human sec
71	30	31.9	27	4	AAM87727	Aam87727 Human imm
72	30	31.9	28	2	AAR10074	Aar10074 Generic s
73	30	31.9	29	2	AAR10077	Aar10077 Example o
74	30	31.9	29	4	AAM18509	Aam18509 Peptide #
75	30	31.9	29	4	ABB37553	Abb37553 Peptide #
76	30	31.9	29	4	AAM30976	Aam30976 Peptide #
77	30	31.9	29	4	ABB32290	Abb32290 Peptide #
78	30	31.9	29	4	ABB22848	Abb22848 Protein #
79	30	31.9	29	4	AAM70664	Aam70664 Human bon
80	30	31.9	29	4	AAM58206	Aam58206 Human bra
81	30	31.9	29	4	ABG52366	Abg52366 Human liv
82	30	31.9	29	4	AAM06090	Aam06090 Peptide #
83	30	31.9	29	5	ABG40354	Abg40354 Human pep
84	30	31.9	30	1	AAP82826	Aap82826 Eel calci
85	30	31.9	30	2	AAR10075	Aar10075 Example o
86	30	31.9	30	2	AAR10076	Aar10076 Example o
87	30	31.9	30	2	AAR10078	Aar10078 Example o
88	30	31.9	30	2	AAR10079	Aar10079 Example o
89	30	31.9	30	2	AAR11695	Aar11695 Calcitoni
90	30	31.9	30	2	AAR11696	Aar11696 Calcitoni
91	30	31.9	30	2	AAR11694	Aar11694 Calcitoni
92	30	31.9	30	2	AAR11697	Aar11697 Calcitoni
93	30	31.9	30	2	AAR11693	Aar11693 Calcitoni
94	30	31.9	30	2	AAR11700	Aar11700 Calcitoni
95	30	31.9	30	2	AAR11699	Aar11699 Calcitoni
96	30	31.9	30	2	AAR11698	Aar11698 Calcitoni
97	30	31.9	30	2	AAR11701	Aar11701 Calcitoni
98	30	31.9	30	2	AAR11702	Aar11702 Calcitoni
99	29.5	31.4	15	6	ABU78506	Abu78506 Novel pro
100	29.5	31.4	15	6	ABU78371	Abu78371 Novel pro
101	29.5	31.4	15	6	ABU78412	Abu78412 Novel pro
102	29.5	31.4	20	6	ABJ38217	Abj38217 Human cyt
103	29.5	31.4	24	2	AAW09791	Aaw09791 Peptide e
104	29	30.9	10	6	ABU75168	Abu75168 Novel pro
105	29	30.9	10	6	ABU77837	Abu77837 Novel pro
106	29	30.9	10	6	ABU77789	Abu77789 Novel pro
107	29	30.9	10	6	ABU73020	Abu73020 Novel pro
108	29	30.9	10	6	ABU75708	Abu75708 Novel pro
109	29	30.9	10	6	ABU77673	Abu77673 Novel pro
110	29	30.9	10	6	ABU73625	Abu73625 Novel pro
111	29	30.9	10	6	ABU76292	Abu76292 Novel pro
112	29	30.9	10	9	ADY51462	Ady51462 HLA-A0201
113	29	30.9	12	2	AAW40636	Aaw40636 Peptide w
114	29	30.9	13	7	ADM75736	Adm75736 Potential
115	29	30.9	13	7	ADM75471	Adm75471 Potential
116	29	30.9	15	6	ABU78370	Abu78370 Novel pro
117	29	30.9	15	6	ABU78338	Abu78338 Novel pro
118	29	30.9	15	6	ABU78436	Abu78436 Novel pro

119	29	30.9	15	6	ABU78524	Abu78524 Novel pro
120	29	30.9	15	6	ABU78491	Abu78491 Novel pro
121	29	30.9	15	6	ADA19559	Ada19559 Measles F
122	29	30.9	15	9	AED14758	Aed14758 Peptide f
123	29	30.9	19	9	ADW11044	Adw11044 Clostridi
124	29	30.9	21	5	ABG66380	Abg66380 IgE Fceps
125	29	30.9	21	5	ABG66372	Abg66372 IgE Fceps
126	29	30.9	21	9	ADV41961	Adv41961 Human pep
127	29	30.9	23	8	ADH34983	Adh34983 N-linked
128	29	30.9	23	10	AEE39364	Aee39364 Human pro
129	29	30.9	23	10	AEE38232	Aee38232 Human ser
130	29	30.9	24	10	AEE39300	Aee39300 Human pro
131	29	30.9	24	10	AEE37898	Aee37898 Human ser
132	29	30.9	25	5	ABG62546	Abg62546 Eubacteri
133	29	30.9	25	5	ABG62664	Abg62664 Eubacteri
134	29	30.9	27	9	ADW11103	Adw11103 Clostridi
135	29	30.9	28	2	AAR11476	Aar11476 Salmon ca
136	29	30.9	29	2	AAW09787	Aaw09787 N-termina
137	29	30.9	29	9	AEB17653	Aeb17653 Drosophil
138	29	30.9	30	2	AAR11475	Aar11475 Eel calci
139	28.5	30.3	15	6	ABU78331	Abu78331 Novel pro
140	28.5	30.3	15	6	ABU78525	Abu78525 Novel pro
141	28.5	30.3	15	6	ABU78559	Abu78559 Novel pro
142	28.5	30.3	15	6	ABP59921	Abp59921 Human neu
143	28.5	30.3	15	7	ADL96067	Adl96067 Human neu
144	28.5	30.3	15	9	ADX02682	Adx02682 Neural th
145	28.5	30.3	18	5	ABJ04211	Abj04211 Kinase-as
146	28.5	30.3	18	6	ABU54258	Abu54258 Eph-B4 pr
147	28.5	30.3	30	10	AEE35960	Aee35960 Human ser
148	28	29.8	9	2	AAY40125	Aay40125 Amino aci
149	28	29.8	9	2	AAY53303	Aay53303 Bcr-Abl e
150	28	29.8	9	2	AAY26641	Aay26641 BCR-ABL-d
151	28	29.8	9	6	ABU76789	Abu76789 Novel pro
152	28	29.8	9	6	ABU76841	Abu76841 Novel pro
153	28	29.8	9	6	ABU73335	Abu73335 Novel pro
154	28	29.8	9	6	ABU75465	Abu75465 Novel pro
155	28	29.8	9	6	ABU76958	Abu76958 Novel pro
156	28	29.8	9	6	ABU76704	Abu76704 Novel pro
157	28	29.8	9	6	ABU76528	Abu76528 Novel pro
158	28	29.8	9	6	ABU76938	Abu76938 Novel pro
159	28	29.8	9	7	ADE68489	Ade68489 Human 161
160	28	29.8	9	7	ADE66008	Ade66008 Human 161
161	28	29.8	9	7	ADE66987	Ade66987 Human 161
162	28	29.8	9	7	ADE68229	Ade68229 Human 161
163	28	29.8	9	7	ADE68118	Ade68118 Human 161
164	28	29.8	9	7	ADE68697	Ade68697 Human 161
165	28	29.8	9	7	ADE68847	Ade68847 Human 161
166	28	29.8	9	7	ADE68916	Ade68916 Human 161
167	28	29.8	9	7	ADE66509	Ade66509 Human 161
168	28	29.8	9	7	ADE66524	Ade66524 Human 161
169	28	29.8	9	7	ADE67224	Ade67224 Human 161
170	28	29.8	9	7	ADE67780	Ade67780 Human 161
171	28	29.8	9	7	ADE68102	Ade68102 Human 161
172	28	29.8	9	7	ADE68311	Ade68311 Human 161
173	28	29.8	9	7	ADE66731	Ade66731 Human 161
174	28	29.8	9	7	ADE66746	Ade66746 Human 161
175	28	29.8	9	7	ADE66240	Ade66240 Human 161
176	28	29.8	9	7	ADE66487	Ade66487 Human 161
177	28	29.8	9	7	ADE68369	Ade68369 Human 161
178	28	29.8	9	7	ADE68490	Ade68490 Human 161
179	28	29.8	10	2	AAR66884	Aar66884 Agonist p

180	28	29.8	10	2	AAW01917	Aaw01917 C140 rece
181	28	29.8	10	4	AAG95140	Aag95140 Human com
182	28	29.8	10	7	ADE66138	Ade66138 Human 161
183	28	29.8	10	7	ADE69482	Ade69482 Human 161
184	28	29.8	10	7	ADE66600	Ade66600 Human 161
185	28	29.8	10	7	ADE66856	Ade66856 Human 161
186	28	29.8	10	7	ADE69292	Ade69292 Human 161
187	28	29.8	10	7	ADE69249	Ade69249 Human 161
188	28	29.8	10	7	ADE67367	Ade67367 Human 161
189	28	29.8	10	7	ADE69899	Ade69899 Human 161
190	28	29.8	10	7	ADE66892	Ade66892 Human 161
191	28	29.8	10	7	ADE66384	Ade66384 Human 161
192	28	29.8	10	7	ADE66679	Ade66679 Human 161
193	28	29.8	10	7	ADE67108	Ade67108 Human 161
194	28	29.8	10	7	ADE69652	Ade69652 Human 161
195	28	29.8	11	2	AAR66883	Aar66883 Agonist p
196	28	29.8	11	2	AAW01916	Aaw01916 C140 rece
197	28	29.8	11	7	ADD23033	Add23033 Breast ca
198	28	29.8	12	3	AAY84189	Aay84189 Amino aci
199	28	29.8	12	8	ADO24729	Ado24729 Mouse lep
200	28	29.8	13	5	ABP63630	Abp63630 Human MHC
201	28	29.8	13	5	AAE27221	Aae27221 Human obe
202	28	29.8	15	3	AAY54775	Aay54775 Human sub
203	28	29.8	15	3	AAY67138	Aay67138 Human pro
204	28	29.8	15	4	AAU38677	Aau38677 Human sub
205	28	29.8	15	5	AAO17727	Aao17727 Human air
206	28	29.8	15	5	ABG91253	Abg91253 Peptide a
207	28	29.8	15	7	ADE70767	Ade70767 Human 161
208	28	29.8	15	7	ADE70471	Ade70471 Human 161
209	28	29.8	15	7	ADE70354	Ade70354 Human 161
210	28	29.8	15	7	ADE70728	Ade70728 Human 161
211	28	29.8	15	7	ADE70110	Ade70110 Human 161
212	28	29.8	15	7	ADE70355	Ade70355 Human 161
213	28	29.8	15	7	ADE70470	Ade70470 Human 161
214	28	29.8	15	7	ADE70504	Ade70504 Human 161
215	28	29.8	15	7	ADE70503	Ade70503 Human 161
216	28	29.8	15	7	ADE70820	Ade70820 Human 161
217	28	29.8	15	8	ADN65557	Adn65557 HLA bindi
218	28	29.8	15	8	ADT07772	Adt07772 Salmon ca
219	28	29.8	17	4	AAM52595	Aam52595 Peptide #
220	28	29.8	17	8	ADV86497	Adv86497 Parathyro
221	28	29.8	18	2	AAR27585	Aar27585 TNF bindi
222	28	29.8	18	2	AAW04312	Aaw04312 Modified
223	28	29.8	18	2	AAW45586	Aaw45586 Peptide f
224	28	29.8	18	3	AAB19656	Aab19656 Streptoco
225	28	29.8	18	6	ABG71717	Abg71717 Antigenic
226	28	29.8	18	8	ADK49420	Adk49420 Human car
227	28	29.8	18	8	ADV86510	Adv86510 Parathyro
228	28	29.8	19	2	AAR26823	Aar26823 Cell adhe
229	28	29.8	20	2	AAR30900	Aar30900 Cell adhe
230	28	29.8	20	2	AAR92724	Aar92724 Immunogen
231	28	29.8	20	3	AAB28456	Aab28456 Murine OB
232	28	29.8	20	3	AAY87734	Aay87734 Murine OB
233	28	29.8	20	3	AAB28475	Aab28475 Murine OB
234	28	29.8	20	5	ABG66603	Abg66603 IgE Fceps
235	28	29.8	20	5	ABB84124	Abb84124 Murine Ob
236	28	29.8	20	6	ABP83487	Abp83487 G protein
237	28	29.8	20	6	ABU64569	Abu64569 Human obe
238	28	29.8	20	8	ADH15364	Adh15364 Gliadin r
239	28	29.8	20	8	ADH16095	Adh16095 Gliadin r
240	28	29.8	20	8	ADH16094	Adh16094 Gliadin r

241	28	29.8	20	8	ADH15365	Adh15365 Gliadin r
242	28	29.8	20	8	ADT93154	Adt93154 Murine ob
243	28	29.8	20	9	AED19923	Aed19923 Canine pa
244	28	29.8	20	9	AEE34588	Aee34588 Wheat gli
245	28	29.8	20	9	AEE34596	Aee34596 Wheat gli
246	28	29.8	20	9	AEE34589	Aee34589 Wheat gli
247	28	29.8	20	9	AEE34597	Aee34597 Wheat gli
248	28	29.8	20	9	AEE34591	Aee34591 Wheat gli
249	28	29.8	20	9	AEE34595	Aee34595 Wheat gli
250	28	29.8	20	9	AEE34592	Aee34592 Wheat gli
251	28	29.8	21	4	ABB42885	Abb42885 Peptide #
252	28	29.8	21	4	AAM36703	Aam36703 Peptide #
253	28	29.8	21	4	AAM76594	Aam76594 Human bon
254	28	29.8	21	4	AAM63781	Aam63781 Human bra
255	28	29.8	21	4	ABG58294	Abg58294 Human liv
256	28	29.8	21	5	ABG45836	Abg45836 Human pep
257	28	29.8	21	5	AAB71448	Aab71448 Human C3
258	28	29.8	22	2	AAR99403	Aar99403 Drosophil
259	28	29.8	22	2	AAW65059	Aaw65059 E. tenell
260	28	29.8	22	5	AAB71462	Aab71462 Human C3
261	28	29.8	24	1	AAP20305	Aap20305 24 residu
262	28	29.8	24	7	ADE03435	Ade03435 BGS-2 leu
263	28	29.8	24	9	ADV55692	Adv55692 G protein
264	28	29.8	24	9	ADV54697	Adv54697 G protein
265	28	29.8	24	9	ADV55693	Adv55693 G protein
266	28	29.8	24	9	ADV54696	Adv54696 G protein
267	28	29.8	25	1	AAP60857	Aap60857 Sequence
268	28	29.8	25	2	AAW09790	Aaw09790 Peptide e
269	28	29.8	25	5	ABG62201	Abg62201 Eubacteri
270	28	29.8	26	6	ABP97145	Abp97145 C-Myc fra
271	28	29.8	26	6	ABP97144	Abp97144 C-Myc fra
272	28	29.8	26	8	ADR84079	Adr84079 S. pyogen
273	28	29.8	27	2	AAW00861	Aaw00861 Anti-obes
274	28	29.8	27	8	ADK49421	Adk49421 Human car
275	28	29.8	27	9	ADV44820	Adv44820 Murine al
276	28	29.8	28	1	AAP82100	Aap82100 Synthetic
277	28	29.8	28	1	AAP82099	Aap82099 Synthetic
278	28	29.8	29	1	AAP80525	Aap80525 Sequence
279	28	29.8	29	1	AAP82107	Aap82107 Synthetic
280	28	29.8	29	1	AAP82108	Aap82108 Synthetic
281	28	29.8	29	2	AAR61495	Aar61495 L-Proline
282	28	29.8	29	2	AAR88115	Aar88115 L-proline
283	28	29.8	29	8	ABO57855	Abo57855 Human gen
284	28	29.8	30	1	AAP40569	Aap40569 Sequence
285	28	29.8	30	1	AAP40567	Aap40567 Sequence
286	28	29.8	30	1	AAP40568	Aap40568 Sequence
287	28	29.8	30	1	AAP82825	Aap82825 Salmon ca
288	28	29.8	30	1	AAP82741	Aap82741 Des-19-le
289	28	29.8	30	1	AAP82740	Aap82740 Des-19-le
290	28	29.8	30	2	AAR07951	Aar07951 Synthetic
291	28	29.8	30	2	AAR07769	Aar07769 Calcium m
292	27	28.7	8	8	ADS97525	Ads97525 Human MEP
293	27	28.7	9	5	ABJ01798	Abj01798 158P1D7 r
294	27	28.7	9	5	ABJ01511	Abj01511 158P1D7 r
295	27	28.7	9	5	ABJ01313	Abj01313 158P1D7 r
296	27	28.7	9	5	ABJ01886	Abj01886 158P1D7 r
297	27	28.7	9	6	ABU76577	Abu76577 Novel pro
298	27	28.7	10	4	AAG95264	Aag95264 Human com
299	27	28.7	10	5	ABJ01936	Abj01936 158P1D7 r
300	27	28.7	10	5	ABJ01461	Abj01461 158P1D7 r
301	27	28.7	10	5	ABJ01361	Abj01361 158P1D7 r

302	27	28.7	10	6	ABU77717	Abu77717 Novel pro
303	27	28.7	10	6	ABU77793	Abu77793 Novel pro
304	27	28.7	10	6	ABU75147	Abu75147 Novel pro
305	27	28.7	10	6	ABU75732	Abu75732 Novel pro
306	27	28.7	10	6	ABU77848	Abu77848 Novel pro
307	27	28.7	10	6	ABR01568	Abr01568 Human ant
308	27	28.7	10	8	ADK03047	Adk03047 Hepatitis
309	27	28.7	10	8	ADK03072	Adk03072 Hepatitis
310	27	28.7	13	4	AAU28716	Aau28716 DPI trypt
311	27	28.7	13	4	AAU28698	Aau28698 DPI trypt
312	27	28.7	13	4	AAU25223	Aau25223 Schizophr
313	27	28.7	13	4	AAB87228	Aab87228 Breast-ca
314	27	28.7	13	4	AAU26346	Aau26346 Depressio
315	27	28.7	13	4	AAU26364	Aau26364 Depressio
316	27	28.7	13	4	AAU15567	Aau15567 Schizophr
317	27	28.7	13	4	ABB52265	Abb52265 Human API
318	27	28.7	13	6	ABR59089	Abr59089 Alzheimer
319	27	28.7	13	8	ADN31903	Adn31903 Human Alz
320	27	28.7	13	8	ADO78834	Ado78834 Schizophr
321	27	28.7	14	1	AAP94363	Aap94363 Part of t
322	27	28.7	14	8	ADT39061	Adt39061 hSARS vir
323	27	28.7	14	8	ADS78481	Ads78481 SARS viru
324	27	28.7	14	8	ADT36591	Adt36591 hSARS vir
325	27	28.7	14	8	ABY00094	Aby00094 SARS coro
326	27	28.7	15	6	ABJ70569	Abj70569 184P1E2-r
327	27	28.7	15	6	ABJ69983	Abj69983 184P1E2-r
328	27	28.7	15	6	ABJ71760	Abj71760 184P1E2-r
329	27	28.7	15	6	ABJ71761	Abj71761 184P1E2-r
330	27	28.7	15	6	ABJ71335	Abj71335 184P1E2-r
331	27	28.7	15	6	ABJ71935	Abj71935 184P1E2-r
332	27	28.7	15	6	ABJ70059	Abj70059 184P1E2-r
333	27	28.7	15	6	ABJ70968	Abj70968 184P1E2-r
334	27	28.7	15	6	ABJ70942	Abj70942 184P1E2-r
335	27	28.7	15	6	ABJ69784	Abj69784 184P1E2-r
336	27	28.7	15	6	ABJ70798	Abj70798 184P1E2-r
337	27	28.7	15	6	ABJ71479	Abj71479 184P1E2-r
338	27	28.7	15	6	ABJ69601	Abj69601 184P1E2-r
339	27	28.7	15	6	ABJ70533	Abj70533 184P1E2-r
340	27	28.7	15	8	ADP26414	Adp26414 Plasmodiu
341	27	28.7	17	4	AAB70776	Aab70776 Human Gra
342	27	28.7	17	4	AAB70777	Aab70777 Human Gra
343	27	28.7	17	9	ADV12720	Adv12720 Human pho
344	27	28.7	18	8	ADP21013	Adp21013 Cottontai
345	27	28.7	18	8	ADP21070	Adp21070 Plant vir
346	27	28.7	18	9	AEE68112	Aee68112 Cottontai
347	27	28.7	19	6	ABR62557	Abr62557 hTid liga
348	27	28.7	19	8	ADG74064	Adg74064 Cottontai
349	27	28.7	19	8	ADP21069	Adp21069 Plant vir
350	27	28.7	19	9	AED02396	Aed02396 Papilloma
351	27	28.7	19	9	AEE68159	Aee68159 Human imm
352	27	28.7	20	4	AAB74840	Aab74840 Human min
353	27	28.7	20	4	AAB67252	Aab67252 Hepatitis
354	27	28.7	20	4	AAM89373	Aam89373 Human imm
355	27	28.7	20	8	ADU79214	Adu79214 Human pep
356	27	28.7	21	8	ADK15980	Adk15980 Human pro
357	27	28.7	22	2	AAR48765	Aar48765 G-protein
358	27	28.7	22	2	AAW02737	Aaw02737 G-protein
359	27	28.7	22	2	AAY27485	Aay27485 E. coli b
360	27	28.7	22	4	AAM15199	Aam15199 Peptide #
361	27	28.7	22	4	AAM27656	Aam27656 Peptide #
362	27	28.7	22	4	AAM67366	Aam67366 Human bon

363	27	28.7	22	4	AAM02939	Aam02939 Peptide #
364	27	28.7	22	5	AAM49327	Aam49327 HIV-1 gp1
365	27	28.7	23	5	AAU86417	Aau86417 Androgen
366	27	28.7	24	8	ADY81099	Ady81099 Rice leaf
367	27	28.7	24	9	ADV25923	Adv25923 SARS coro
368	27	28.7	25	2	AAY33334	Aay33334 P. monodo
369	27	28.7	25	3	AAB22956	Aab22956 Tiger pra
370	27	28.7	25	3	AAY93925	Aay93925 N-termina
371	27	28.7	25	4	AAE07931	Aae07931 N-termina
372	27	28.7	25	5	AAO21348	Aao21348 Panaeus m
373	27	28.7	25	6	ABP99568	Abp99568 Human sec
374	27	28.7	25	9	ADY81712	Ady81712 Krill-der
375	27	28.7	25	10	AEE39235	Aee39235 Human ser
376	27	28.7	26	2	AAW01183	Aaw01183 Serine pr
377	27	28.7	26	3	AAB39185	Aab39185 Human sec
378	27	28.7	26	4	AAB50579	Aab50579 Flea seri
379	27	28.7	27	2	AAR25352	Aar25352 Calcitoni
380	27	28.7	27	4	ABB36341	Abb36341 Peptide #
381	27	28.7	27	4	ABB31146	Abb31146 Peptide #
382	27	28.7	27	5	ABG39127	Abg39127 Human pep
383	27	28.7	27	7	ADK14963	Adk14963 Urinary s
384	27	28.7	27	7	ADL66715	Adl66715 Shg prote
385	27	28.7	27	8	ABO60614	Abo60614 Human gen
386	27	28.7	28	3	AAB22001	Aab22001 Human V g
387	27	28.7	28	5	AAE23914	Aae23914 Human TCR
388	27	28.7	28	10	AEE28088	Aee28088 N. mening
389	27	28.7	29	2	AAR30298	Aar30298 [Nva 0,Le
390	27	28.7	29	2	AAR30286	Aar30286 [Val 0,Le
391	27	28.7	29	2	AAR30333	Aar30333 [Ala 0, L
392	27	28.7	29	2	AAR30292	Aar30292 [Thr 0,Le
393	27	28.7	29	2	AAR30325	Aar30325 [Ile 0, L
394	27	28.7	29	2	AAR30329	Aar30329 [Thr 0, L
395	27	28.7	29	2	AAR30335	Aar30335 [Nva 0, L
396	27	28.7	29	2	AAR30296	Aar30296 [Ala 0,Le
397	27	28.7	29	2	AAR30323	Aar30323 [Val 0, L
398	27	28.7	29	2	AAR30337	Aar30337 [Nle 0, L
399	27	28.7	29	2	AAR30331	Aar30331 [Ser 0, L
400	27	28.7	29	2	AAR30290	Aar30290 [Met 0,Le
401	27	28.7	29	2	AAR30284	Aar30284 [Leu 0,8,
402	27	28.7	29	2	AAR30294	Aar30294 [Ser 0,Le
403	27	28.7	29	2	AAR30321	Aar30321 [Leu 0,8,
404	27	28.7	29	2	AAR30327	Aar30327 [Met 0, L
405	27	28.7	29	2	AAR30288	Aar30288 [Ile 0,Le
406	27	28.7	29	2	AAR30300	Aar30300 [Nle 0,Le
407	27	28.7	29	4	AAU27336	Aau27336 Novel bon
408	27	28.7	29	5	AAE13588	Aae13588 Glutathio
409	27	28.7	29	8	ADT41179	Adt41179 hSARS vir
410	27	28.7	29	8	ADS80594	Ads80594 SARS viru
411	27	28.7	29	8	ADT38709	Adt38709 hSARS vir
412	27	28.7	29	8	ADU99091	Adu99091 Human 109
413	27	28.7	29	8	ADU99088	Adu99088 Human 109
414	27	28.7	29	9	AEB27671	Aeb27671 pGEX-KG v
415	27	28.7	29	9	AEC65508	Aec65508 Human 109
416	27	28.7	29	9	AEC65505	Aec65505 Human 109
417	27	28.7	30	8	ADX95629	Adx95629 Plant ful
418	27	28.7	30	9	AEE68223	Aee68223 Cottontai
419	26.5	28.2	22	5	ABG37670	Abg37670 Human pep
420	26.5	28.2	22	9	AEE22843	Aee22843 Human IL-
421	26.5	28.2	24	10	AEE37361	Aee37361 Human ser
422	26.5	28.2	28	9	AEE22851	Aee22851 Human IL-
423	26	27.7	7	7	ADE78015	Ade78015 Synthetic

424	26	27.7	9	4	AAE09516	Aae09516 Human muc
425	26	27.7	9	4	AAE09517	Aae09517 Human muc
426	26	27.7	9	4	AAU00554	Aau00554 Human MUC
427	26	27.7	9	6	ABR19018	Abr19018 Human can
428	26	27.7	9	7	ADE69119	Ade69119 Human 161
429	26	27.7	9	7	ADE78017	Ade78017 Synthetic
430	26	27.7	9	10	AEE60582	Aee60582 Human MUC
431	26	27.7	10	6	ABR19119	Abr19119 Human can
432	26	27.7	10	6	ABR19695	Abr19695 Human can
433	26	27.7	10	6	ABR19958	Abr19958 Human can
434	26	27.7	10	6	ABR19296	Abr19296 Human can
435	26	27.7	10	6	ABR18879	Abr18879 Human can
436	26	27.7	10	6	ABJ67340	Abj67340 184P1E2-r
437	26	27.7	10	6	ABJ66616	Abj66616 184P1E2-r
438	26	27.7	10	6	ABJ65906	Abj65906 184P1E2-r
439	26	27.7	10	6	ABJ69262	Abj69262 184P1E2-r
440	26	27.7	10	6	ABJ68663	Abj68663 184P1E2-r
441	26	27.7	10	6	ABJ67896	Abj67896 184P1E2-r
442	26	27.7	10	6	AAE38125	Aae38125 Human cyt
443	26	27.7	10	7	ADE69291	Ade69291 Human 161
444	26	27.7	10	7	ADE66672	Ade66672 Human 161
445	26	27.7	10	7	ADE66920	Ade66920 Human 161
446	26	27.7	10	7	ADE66364	Ade66364 Human 161
447	26	27.7	10	7	ADW33062	Adw33062 HLA bindi
448	26	27.7	11	2	AAR32183	Aar32183 Ranakinin
449	26	27.7	11	5	ABG67301	Abg67301 Human ADP
450	26	27.7	11	6	ABP74753	Abp74753 Proteome
451	26	27.7	11	6	ABR75650	Abr75650 Liver res
452	26	27.7	11	6	ADA23401	Ada23401 Alzheimer
453	26	27.7	11	7	ADN07371	Adn07371 Liver res
454	26	27.7	13	2	AAW37160	Aaw37160 Human TcA
455	26	27.7	13	7	ADD43994	Add43994 CPG2 pept
456	26	27.7	13	10	AEE30765	Aee30765 Represent
457	26	27.7	13	10	AEF52381	Aef52381 Interfaci
458	26	27.7	14	1	AAP91703	Aap91703 Human tum
459	26	27.7	14	2	AAR57740	Aar57740 Human tum
460	26	27.7	14	5	AAB71445	Aab71445 Human C3
461	26	27.7	14	6	ABP59644	Abp59644 R ruber a
462	26					

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AC   AAW54070;
XX
DT   10-AUG-1998  (first entry)
XX
DE   IVI-4 protein fragment of E. faecalis.
XX
KW   IVI-2 locus; ivi-3 protein; ivi-4 protein; transcriptional regulator;
KW   antibiotic testing; infection; endocarditis; therapy.
XX
OS   Enterococcus faecalis.
XX
PN   WO9812205-A1.
XX
PD   26-MAR-1998.
XX
PF   18-SEP-1997;   97WO-US016589.
XX
PR   18-SEP-1996;   96US-0025899P.
XX
PA   (VIRU-) VIRUS RES INST INC.
XX
PI   Beattie DT;
XX
DR   WPI; 1998-217198/19.
DR   N-PSDB; AAV24034.
XX
PT   Enterococcus faecalis transcriptional regulators ivi-2 and ivi-3, and ivi
PT   -4 - useful to test antibiotics, to identify pharmaceuticals for treating
PT   or controlling E. faecalis infections, particularly endocarditis.
XX
PS   Claim 1; Fig 1; 36pp; English.
XX
CC   This sequence is a ivi-4 fragment from Enterococcus faecalis. It is
CC   encoded by the DNA sequence of the invention, which encodes the mature
CC   ivi-2, and ivi-3 proteins, and also contains a partial ivi-4 protein
CC   coding sequence. Ivi-2 and ivi-3 are Enterococcus faecalis
CC   transcriptional regulator ivi-2 or ivi-3. Ivi-2 and ivi-3 can be used as
CC   reagents for testing antibiotics for their activity in deactivating or
CC   controlling their activity as part of a screening process to identify
CC   pharmaceuticals for treating or controlling E. faecalis infections,
CC   particularly endocarditis. The DNA sequence can be used in the generation
CC   of antisense oligonucleotides or probes for the treatment and
CC   identification of E. faecalis infection. The products are also useful as
CC   in vitro agents for producing monoclonal antibodies, useful in diagnostic
CC   and screening procedures for identifying or treating E. faecalis
CC   infections
XX
SQ   Sequence 28 AA;

  Query Match             35.1%;  Score 33;  DB 2;  Length 28;
  Best Local Similarity   62.5%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 LELMPNIE 17
              ||:|||::
Db         12 LEIMPNVK 19
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Q8L2T5_NEIME
ID   Q8L2T5_NEIME   PRELIMINARY;   PRT;    18 AA.
AC   Q8L2T5;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 6.
DE   Tryptophan transporter (Fragment).
OS   Neisseria meningitidis.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC   Neisseriaceae; Neisseria.
OX   NCBI_TaxID=487;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=126E;
RX   MEDLINE=22051050; PubMed=12055303;
RA   Zhu P., Klutch M.J., Bash M.C., Tsang R.S.W., Ng L.K., Tsai C.M.;
RT   "Genetic diversity of three lgt loci for biosynthesis of
RT   lipooligosaccharide (LOS) in Neisseria species.";
RL   Microbiology 148:1833-1844(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF470685; AAM33537.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   18 AA;  1944 MW;  08DE06F3E9B8C27E CRC64;

  Query Match             41.5%;  Score 39;  DB 2;  Length 18;
  Best Local Similarity   35.7%;  Pred. No. 82;
  Matches    5;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 NLSSDIIGQLELMP 14
              |::: :: |:||:|
Db          1 NIAAQVLSQMELVP 14
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 Sequence 530, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
;  APPLICANT: EDWARDS, ALED
;  APPLICANT:  DHARAMSI, AKIL
;  APPLICANT:  VEDADI, MASOUD
;  TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
;  FILE REFERENCE: IPT-330.01
;  CURRENT APPLICATION NUMBER: US/11/122,986
;  CURRENT FILING DATE:  2005-05-05
;  PRIOR APPLICATION NUMBER: 60/423,875
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,832
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,915
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,757
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/423,758
;  PRIOR FILING DATE: 2002-11-05
;  PRIOR APPLICATION NUMBER: 60/424,367
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,376
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,370
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,362
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/424,373
;  PRIOR FILING DATE: 2002-11-06
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 844
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 530
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-11-122-986-530

  Query Match             27.7%;  Score 26;  DB 7;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 NIERF 19
              |||||
Db          1 NIERF 5
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 Sequence 41, Application US/10147140
; Publication No. US20030153730A1
; GENERAL INFORMATION:
;  APPLICANT: STRACKE, MARY
;  APPLICANT:  LIOTTA, LANCE
;  APPLICANT:  SCHIFFMANN, ELLIOTT
;  APPLICANT:  KRUTZCH, HENRY
;  APPLICANT:  MURATA, JUN
;  TITLE OF INVENTION: AUTOTAXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
;  TITLE OF INVENTION:  CANCER DIAGNOSIS AND THERAPY
;  FILE REFERENCE: 2026-4149US4
;  CURRENT APPLICATION NUMBER: US/10/147,140
;  CURRENT FILING DATE:  2002-05-15
;  PRIOR APPLICATION NUMBER: 07/822,043
;  PRIOR FILING DATE: 1992-01-17
;  PRIOR APPLICATION NUMBER: 08/249,182
;  PRIOR FILING DATE: 1994-05-25
;  PRIOR APPLICATION NUMBER: 08/346,455
;  PRIOR FILING DATE: 1994-11-28
;  PRIOR APPLICATION NUMBER: 08/977,221
;  PRIOR FILING DATE: 1997-11-24
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-10-147-140-41

  Query Match             31.9%;  Score 30;  DB 4;  Length 7;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+06;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 LMPNIER 18
              :|||||:
Db          1 VMPNIEK 7
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 Sequence 40, Application US/10161097
; Publication No. US20030096404A1
; GENERAL INFORMATION:
;  APPLICANT: ROSENZWEIG, Michael
;  APPLICANT:  PYKETT, Mark J.
;  APPLICANT:  SCADDEN, David T.
;  APPLICANT:  POZNANSKY, Mark C.
;  TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
;  TITLE OF INVENTION:  FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
;  TITLE OF INVENTION:  DEVICES
;  FILE REFERENCE: C1005/7012/KA/ERG
;  CURRENT APPLICATION NUMBER: US/10/161,097
;  CURRENT FILING DATE:  2002-05-31
;  PRIOR APPLICATION NUMBER: US/09/574,749
;  PRIOR FILING DATE: 2002-05-31
;  PRIOR APPLICATION NUMBER: US 60/107,972
;  PRIOR FILING DATE: 1998-11-12
;  PRIOR APPLICATION NUMBER: PCT/US99/26795
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: US 09/524,749
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Measles source
US-10-161-097-40

  Query Match             30.9%;  Score 29;  DB 4;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 9e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 LELMPNI 16
              ::|||||
Db          6 IKLMPNI 12
```

```
 Sequence 7, Application US/09147857
; Patent No. 6376235
; GENERAL INFORMATION:
;  APPLICANT:  Beattie, David T.
;  TITLE OF INVENTION:  IVI-2, IVI-3 and IVI-4 Loci of Enterococcus Faecalis
;  TITLE OF INVENTION:  Polynucleotide, Polypeptides and Method of Use Therefor
;  FILE REFERENCE:  732250-215
;  CURRENT APPLICATION NUMBER: US/09/147,857
;  CURRENT FILING DATE:  1999-03-16
;  PRIOR APPLICATION NUMBER:  U.S. 60/025,899
;  PRIOR FILING DATE:  1996-09-18
;  PRIOR APPLICATION NUMBER:  PCT/US97/16589
;  PRIOR FILING DATE:  1997-09-18
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 28
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Deduced amino
;   OTHER INFORMATION: acid sequence of a portion of IVI-4 polypeptide
US-09-147-857-7

  Query Match             35.1%;  Score 33;  DB 2;  Length 28;
  Best Local Similarity   62.5%;  Pred. No. 82;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 LELMPNIE 17
               ||:|||:: 
Db          12 LEIMPNVK 19
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_519_537
Perfect score: 94
Sequence: 1 NLSSDIIGQLELMPNIERF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94	100.0	19	9	ADW11046	Adw11046 Clostridi
2	94	100.0	27	9	ADW11104	Adw11104 Clostridi
3	47	50.0	27	9	ADW11105	Adw11105 Clostridi
4	38	40.4	24	2	AAR84289	Aar84289 Aq. elcat
5	37	39.4	30	2	AAR07952	Aar07952 Synthetic

```
 Sequence 40, Application US/09574749B
; Patent No. 6548299
; GENERAL INFORMATION:
;  APPLICANT: ROSENZWEIG, Michael
;  APPLICANT:  PYKETT, Mark J.
;  APPLICANT:  SCADDEN, David T.
;  APPLICANT:  POZNANSKY, Mark C.
;  TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
;  TITLE OF INVENTION:  FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
;  TITLE OF INVENTION:  DEVICES
;  FILE REFERENCE: C1005/7012/KA/ERG
;  CURRENT APPLICATION NUMBER: US/09/574,749B
;  CURRENT FILING DATE:  2002-05-31
;  PRIOR APPLICATION NUMBER: US 60/107,972
;  PRIOR FILING DATE: 1998-11-12
;  PRIOR APPLICATION NUMBER: PCT/US99/26795
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: US 09/524,749
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Measles source
US-09-574-749B-40

  Query Match           30.9%;  Score 29;  DB 2;  Length 15;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 LELMPNI 16
              ::|||||
Db          6 IKLMPNI 12
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Sequence 44, Application US/08433522A
; Patent No. 6013514
;  GENERAL INFORMATION:
;    APPLICANT:  CHONG, Pele
;    APPLICANT:  THOMAS, Wayne
;    APPLICANT:  YANG, Yan Ping
;    APPLICANT:  LOOSMORE, Sheena
;    APPLICANT:  SIA, Dwo Yuan Charles
;    APPLICANT:  KLEIN, Michel
;    TITLE OF INVENTION:  HAEMOPHILUS OUTER MEMBRANE PROTEIN
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  6TH Floor, 330 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/433,522A
;      FILING DATE:  12-SEP-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEWART, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-434 MIS:jb
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-433-522A-44

  Query Match             30.9%;  Score 29;  DB 2;  Length 27;
  Best Local Similarity   71.4%;  Pred. No. 3.9e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 LSSDIIG 8
              :|||:||
Db         21 ISSDVIG 27
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:30:50 ; Search time 99.3 Seconds
(without alignments)
176.992 Million cell updates/sec

Title: US-10-821-669-1_COPY_533_551
Perfect score: 105
Sequence: 1 NIERFPNGKKYELDKYTMF 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 37017

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	36	34.3	19	2	Q4Z5V1_PLABE	Q4z5v1 plasmodium
2	34.5	32.9	26	2	Q4YE51_PLABE	Q4ye51 plasmodium
3	33	31.4	23	2	Q4XN62_PLACH	Q4xn62 plasmodium

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RESULT 19
US-10-334-726-299
; Sequence 299, Application US/10334726
; Publication No. US20030211521A1
; GENERAL INFORMATION:
;  APPLICANT: TAYLOR-PAPADIMITROU, JOYCE
;  TITLE OF INVENTION: BREAST CANCER ANTIGEN
;  FILE REFERENCE: 1090-36
;  CURRENT APPLICATION NUMBER: US/10/334,726
;  CURRENT FILING DATE:  2003-01-02
;  PRIOR APPLICATION NUMBER: US/09/645,446
;  PRIOR FILING DATE: 2000-08-25
;  PRIOR APPLICATION NUMBER: PCT/GB99/00866
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: GB 9805877.9
;  PRIOR FILING DATE: 1998-09-20
;  NUMBER OF SEQ ID NOS: 324
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 299
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:predicted
;   OTHER INFORMATION: peptide
US-10-334-726-299

  Query Match             30.5%;  Score 32;  DB 4;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1.9e+06;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ERFPNGKK 10
              |  |||||
Db          1 EPLPNGKK 8
```

```
Sequence 8, Application US/09925442
; Patent No. US20020103346A1
;   GENERAL INFORMATION:
;        APPLICANT: VOGEL, CARL-WILHELM
;                   BREDEHORST, REINHORST
;                   KOCK, MICHAEL
;                   FRITZINGER, DAVID
;        TITLE OF INVENTION: RECOMBINANT PROCVF
;        NUMBER OF SEQUENCES: 39
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;                        P.C.
;             STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22202
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/925,442
;             FILING DATE: 10-Aug-2001
;             CLASSIFICATION:
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/017,947
;             FILING DATE:
;        ATTORNEY/AGENT INFORMATION:
;             NAME: OBLON, NORMAN F.
;             REGISTRATION NUMBER: 24,618
;             REFERENCE/DOCKET NUMBER: 1126-0107-0X
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-413-3000
;             TELEFAX: 703-413-2220
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 30 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-925-442-8
```

533-551

```
  Query Match             30.5%;  Score 32;  DB 3;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 KYELDK 15
               ||||||
Db           7 KYELDK 12
```

```
Sequence 51, Application US/08447411
; Patent No. 5773243
;  GENERAL INFORMATION:
;    APPLICANT:  FRITZINGER, DAVID C.
;    APPLICANT:  BREDEHORST, REINHARD
;    APPLICANT:  VOGEL, CARL-WILHELM
;    TITLE OF INVENTION:  DNA ENCODING COBRA C3, CVF1, AND CVF2
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,411
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/043,747
;      FILING DATE:  07-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5773243man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1126-101-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-447-411-51

  Query Match             30.5%;  Score 32;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 KYELDK 15
              ||||||
Db          7 KYELDK 12
```

```
Sequence 8, Application US/08662227
; Patent No. 5922320
;  GENERAL INFORMATION:
;    APPLICANT:  VOGEL, CARL-WILHELM
;    APPLICANT:  BREDEHORST, REINHORST
;    APPLICANT:  KOCK, MICHAEL
;    APPLICANT:  FRITZINGER, DAVID
;    TITLE OF INVENTION:  RECOMBINANT PROCVF
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/662,227
;      FILING DATE:  14-JUN-1996
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  1126-0107-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-662-227-8

  Query Match          30.5%;  Score 32;  DB 1;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 3.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 KYELDK 15
              ||||||
Db          7 KYELDK 12
```

OS Hepatitis C virus.
OS Synthetic.
XX
PN WO2004069864-A1.
XX
PD 19-AUG-2004.
XX
PF 29-DEC-2003; 2003WO-FR003922.
XX
PR 07-JAN-2003; 2003FR-00000094.
XX
PA (INMR) BIOMERIEUX SA.
PA (CNRS) CENT NAT RECH SCI.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
XX
PI Bain C, Inchauspe G, Lavergne J, Parroche P, Penin F;
XX
DR WPI; 2004-625448/60.
XX
PT New immunogenic polypeptide form hepatitis C virus, useful for treatment,
PT prevention and diagnosis of infection, also related epitopes, nucleic
PT acids and antibodies.
XX
PS Claim 12; SEQ ID NO 298; 231pp; French.
XX
CC The present invention describes polypeptide F' (I) that induces an immune
CC response against the hepatitis C virus (HCV) and comprises the 99 amino
CC acids (aa) present between positions 43 and 141 of the HCV polyprotein.
CC Also described: (1) nucleic acid sequences (II) that encode (I); (2) an
CC epitope (E) that induces a response against HCV and comprises the 9 aa
CC between positions 40 and 48, 43 and 51, 50 and 58 or 73 and 81 of the HCV
CC polyprotein; (3) nucleic acid sequences (IIa) that encode (E); (4) an
CC expression vector that contains (II) or (IIa), or two (IIa), and
CC necessary expression elements; (5) microorganisms or host cells
CC transformed by at least one vector of (4); (6) antibodies (Ab) directed
CC against (I) or (E); and (7) a method for the detection and/or
CC quantification of HCV using Ab. (I) has virucide, hepatotropic and
CC antiinflammatory activities, and can be used in vaccines. (I) induces a
CC cell-mediated response in subjects seropositive for HCV and particularly
CC secretion of interleukin-10, optionally also of interferon-gamma. They
CC are effective in patients infected with viral genotypes 1b and 3,
CC whatever their HLA type. (I) and their epitopes can be used to inhibit,
CC prevent or treat hepatitis C virus infection in animals, especially
CC humans, particularly as vaccines, and including where nucleic acid
CC sequences (II), or vectors containing them, are used to express (I) or
CC (E). The method can particularly be used in subjects who do not respond
CC well to treatment with interferon and ribavirine. (I), (II) and
CC antibodies directed against (I) or (E), can be used for diagnostic
CC determination and/or quantification of HCV, in vitro. The present
CC sequence represents an anti-HCV immunogenic protein F' epitope peptide,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 9 AA;

Query Match 30.5%; Score 32; DB 8; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.1e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 RFPNGKK 10
              |||:|:|
Db          1 RFPSGRK 7
```

RESULT 46
ADZ75857
ID ADZ75857 standard; peptide; 21 AA.
XX
AC ADZ75857;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human non-selenium glutathione peroxidase (NSGP) antigenic peptide SEQ:2.
XX
KW Diagnosis; oxidative stress; neurodegenerative disease;
KW neurological disease; Alzheimers disease; Parkinsons disease; dementia;
KW non-selenium glutathione peroxidase; Ca2+-independent phospholipase A2;
KW antigen.
XX
OS Homo sapiens.
XX
PN US2005100979-A1.
XX
PD 12-MAY-2005.
XX
PF 29-AUG-2003; 2003US-00651056.
XX
PR 30-SEP-2002; 2002AU-00951775.
XX
PA (POWE/) POWER J H T.
XX
PI Power JHT;
XX
DR WPI; 2005-365635/37.
XX
PT Diagnosing a disease state associated with oxidative stress, for
PT detecting or treating neurodegenerative disease, comprises measuring the
PT level of non-selenium glutathione peroxidase protein in a biological
PT fluid or tissue.
XX
PS Claim 14; SEQ ID NO 2; 17pp; English.
XX
CC The invention relates to a method of diagnosing a disease state
CC associated with oxidative stress by measuring the level of non-selenium
CC glutathione peroxidase (NSGP, also known as lysosomal type Ca2+-
CC independent phospholipase A2) protein in a biological fluid or tissue
CC obtained from a patient. The level of NSGP protein may be compared to a
CC control, or may be measured in samples taken from the patient over a
CC period of time, and is preferably determined using an NSGP-specific
CC antibody. An increase in the level of NSGP protein measured is indicative
CC of neuronal oxidative stress, which has been implicated as a cause of
CC neurodegenerative diseases such as Alzheimer's disease, Parkinson's
CC disease and dementia. The invention also relates to NSGP-specific
CC antibodies raised against one of two specific NSGP peptide fragments
CC (ADZ75856-ADZ75857, and a method of detecting oxidative stress in an
CC individual using NSGP-specific antibodies. The invention further
CC discloses methods for producing NSGP-specific antibodies, an immunogenic
CC composition comprising the NSGP peptide fragments ADZ75856-ADZ75857, and
CC a method for inhibiting or alleviating one or more symptoms of a
CC neurodegenerative disease using a substance that upregulates NSGP
CC expression or mimics its activity. The methods of the invention are
CC useful for the diagnosis of oxidative stress or a disease related to
CC oxidative stress, especially Alzheimer's disease, Parkinson's disease and
CC dementia. The present sequence represents a specifically claimed C-

CC terminal antigenic peptide fragment of human NSGP (corresponding to
CC residues 199-219 of NSGP, ADZ75858) that is recognized by antibodies of
CC the invention.
XX
SQ Sequence 21 AA;

Query Match 30.5%; Score 32; DB 9; Length 21;
Best Local Similarity 55.6%; Pred. No. 7.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 ERFPNGKKY 11
              :  |:||||
Db         11 KELPSGKKY 19
```

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_547_565
Perfect score: 105
Sequence: 1 KYTMFHYLRAQEFEHGKSR 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	105	100.0	19	9	ADW11048	Adw11048 Clostridi
2	105	100.0	27	9	ADW11106	Adw11106 Clostridi
3	52	49.5	27	9	ADW11105	Adw11105 Clostridi
4	49	46.7	27	9	ADW11107	Adw11107 Clostridi
5	47	44.8	8	9	ADZ69794	Adz69794 Botulinum
6	43	41.0	13	5	ABG97927	Abg97927 Human INF

```
ADH78637
ID   ADH78637 standard; peptide; 15 AA.
XX
AC   ADH78637;
XX
DT   15-APR-2004  (first entry)
XX
DE   Human fibroblast interferon-beta protein based peptide, SEQ ID No 45.
XX
KW   T-cell epitope; cytokine; receptor; CD4+; CD8+; immunogenicity;
KW   interferon-beta; tumour necrosis factor receptor-1; erythropoietin;
KW   thrombopoietin; inflammation; cancer; anaemia;
KW   human fibroblast interferon-beta.
XX
OS   Homo sapiens.
XX
PN   WO2003104263-A2.
XX
PD   18-DEC-2003.
XX
PF   26-FEB-2003; 2003WO-US005917.
XX
PR   01-MAY-2002; 2002US-0376743P.
XX
PA   (GEMV ) GENENCOR INT INC.
XX
PI   Harding FA,  Power SD;
XX
DR   WPI; 2004-062306/06.
XX
PT   Determining T-cell epitope of a protein (e.g. cytokine or cytokine
PT   receptor), useful for reducing protein allergenicity, comprises combining
PT   differentiated dendritic cells and naive T-cells with a peptide having
PT   the T-cell epitope.
XX
PS   Example 2; SEQ ID NO 45; 51pp; English.
XX
CC   The invention relates to a novel method for determining a T-cell epitope
CC   of a protein, where the protein is selected from cytokines and cytokine
CC   receptors. The method comprises combining a solution of differentiated
CC   dendritic cells and naive CD4+ and/or CD8+ T-cells with a pepset of
CC   peptides comprising the T-cell epitope. The composition and methods are
CC   useful in reducing the immunogenicity of cytokines and cytokine receptors
CC   such as interferon-beta, soluble tumour necrosis factor receptor-1,
CC   erythropoietin or thrombopoietin. These modified cytokines and cytokine
CC   receptors may be used for treating various conditions such as
CC   inflammation, cancer or anaemia. This sequence represents a peptide based
CC   on the human fibroblast interferon-beta protein sequence of the
CC   invention.
XX
SQ   Sequence 15 AA;

  Query Match             32.4%;  Score 34;  DB 8;  Length 15;
  Best Local Similarity   62.5%;  Pred. No. 97;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQEF 13
              |||:|:|:
Db          2 HYLKAKEY 9
```

```
Q08578_HUMAN
ID   Q08578_HUMAN   PRELIMINARY;   PRT;    27 AA.
AC   Q08578;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 19.
DE   Complement receptor (Fragment).
GN   Name=CR2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93018869; PubMed=1383386; DOI=10.1084/jem.176.5.1405;
RA   Birkenbach M., Tong X., Brandbury L.E., Tedder T.F., Kieff E.;
RT   "Characterization of a epstein-bar virus receptor on human epithelial
RT   cells.";
RL   J. Exp. Med. 176:1405-1414(1992).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; X68990; CAA48779.1; -; mRNA.
DR   PIR; I37261; I37261.
DR   GO; GO:0004872; F:receptor activity; IEA.
KW   Receptor.
FT   NON_TER       1      1
FT   NON_TER      27     27
SQ   SEQUENCE   27 AA;  2912 MW;  8A12201A98A6DA60 CRC64;

  Query Match             27.6%;  Score 29;  DB 2;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 2.5e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQ 11
              |||||:
Db          9 HYLRAR 14
```

```
Sequence 5, Application US/09029052A
; Patent No. 6140043
; GENERAL INFORMATION:
;  APPLICANT: Dierich, Manfred P
;  APPLICANT: Chen, Ying Hua
;  TITLE OF INVENTION: Pharmaceutical compositions for competitively
;  TITLE OF INVENTION: inhibiting the binding of a retrovirus to the
;  TITLE OF INVENTION: IFN-receptor and means for diagnosis of an HIV
;  TITLE OF INVENTION: infection.
;  FILE REFERENCE: 147-169P
;  CURRENT APPLICATION NUMBER: US/09/029,052A
;  CURRENT FILING DATE: 1998-04-20
;  EARLIER APPLICATION NUMBER: PCT/EP96/03648
;  EARLIER FILING DATE: 1995-08-18
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Source of Artificial Sequence: synthesized from
;   OTHER INFORMATION: the human IFN-beta receptor binding region 2
;   OTHER INFORMATION: (aa123-140)
US-09-029-052-5

  Query Match             41.0%;  Score 43;  DB 2;  Length 18;
  Best Local Similarity   50.0%;  Pred. No. 0.55;
  Matches    6;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MFHYLRAQEFEH 15
              : |||:|:|: |
Db          5 ILHYLKAKEYSH 16
```

```
Sequence 103, Application US/10038612
; Patent No. 6723830
; GENERAL INFORMATION:
;  APPLICANT: Ben-Sasson, Shmuel A.
;  TITLE OF INVENTION: Short Peptides Which Selectively
;  TITLE OF INVENTION:  Modulate the Activity of Protein Kinases
;  FILE REFERENCE: 1242.1029-000 (CMCC-679)
;  CURRENT APPLICATION NUMBER: US/10/038,612
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US 09/161,094
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 172
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 103
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: MYRISTATE
;   LOCATION: (1)...(0)
;   NAME/KEY: AMIDATION
;   LOCATION: (0)...(21)
;   OTHER INFORMATION: c-Sea
US-10-038-612-103

  Query Match             30.5%;  Score 32;  DB 2;  Length 21;
  Best Local Similarity   71.4%;  Pred. No. 61;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQE 12
              |::||||
Db         12 HFIRAQE 18
```

```
Sequence 113, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
;  GENERAL INFORMATION:
;    APPLICANT:  Dower, William J.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Cwirla, Steven E.
;    APPLICANT:  Gates, Christian
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Balasubramanian, Palaniappan
;    APPLICANT:  Wagstrom, Christopher R.
;    APPLICANT:  Hendren, Richard W.
;    APPLICANT:  Deprince, Randolph B.
;    APPLICANT:  Podduturi, Surekha
;    APPLICANT:  Yin, Qun
;    TITLE OF INVENTION:  PEPTIDES AND COMPOUNDS THAT BIND TO A
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  244
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Glaxo Wellcome
;      STREET:  Five Moore Drive, P.O. Box 13398
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/764,640
;      FILING DATE:  11-DEC-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hrubiec, Robert T.
;      REGISTRATION NUMBER:  36,392
;      REFERENCE/DOCKET NUMBER:  PK3281
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-248-1000
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-764-640-113

  Query Match             29.5%;  Score 31;  DB 1;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 39;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 QEFEHG 16
               |||:||
Db           4 QEFKHG 9
```

```
 Sequence 113, Application US/09244298A
; Patent No. 6121238
;  GENERAL INFORMATION:
;    APPLICANT:  Dower, William J.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Cwirla, Steven E.
;    APPLICANT:  Gates, Christian
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Balasubramanian, Palaniappan
;    APPLICANT:  Wagstrom, Christopher R.
;    APPLICANT:  Hendren, Richard W.
;    APPLICANT:  Deprince, Randolph B.
;    APPLICANT:  Podduturi, Surekha
;    APPLICANT:  Yin, Qun
;    TITLE OF INVENTION:  PEPTIDES AND COMPOUNDS THAT BIND TO A
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  244
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Glaxo Wellcome
;      STREET:  Five Moore Drive, P.O. Box 13398
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/244,298A
;      FILING DATE:  11-DEC-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hrubiec, Robert T.
;      REGISTRATION NUMBER:  36,392
;      REFERENCE/DOCKET NUMBER:  PK3281
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-248-1000
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-244-298A-113

  Query Match             29.5%;  Score 31;  DB 2;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 39;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 QEFEHG 16
              |||:||
Db          4 QEFKHG 9
```

```
Sequence 69, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 548-555)
US-10-715-810-69

  Query Match             44.8%;  Score 47;  DB 5;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YTMFHYLR 9
              ||||||||
Db          1 YTMFHYLR 8
```

```
Sequence 76, Application US/10471894B
; Publication No. US20050054052A1
; GENERAL INFORMATION:
;  APPLICANT: Carr, Francis J.
;  APPLICANT:  Carter, Graham
;  APPLICANT:  Jones, Tim
;  APPLICANT:  Watkins, John
;  APPLICANT:  Baker, Matthew
;  TITLE OF INVENTION: MODIFIED INTERFERON BETA WITH REDUCED
;  TITLE OF INVENTION:  IMMUNOGENICITY
;  FILE REFERENCE: MER-124
;  CURRENT APPLICATION NUMBER: US/10/471,894B
;  CURRENT FILING DATE:  2003-09-12
;  PRIOR APPLICATION NUMBER: PCT/EP02/02925
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: EP 01106539.8
;  PRIOR FILING DATE: 2001-03-15
;  NUMBER OF SEQ ID NOS: 141
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 13
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MHC class II binding epitope
US-10-471-894B-76

  Query Match             40.0%;  Score 42;  DB 5;  Length 13;
  Best Local Similarity   60.0%;  Pred. No. 8.6;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 HYLRAQEFEH 15
              |||:|:|: |
Db          1 HYLKAKEYSH 10
```

```
Sequence 141, Application US/10820467
; Publication No. US20050054053A1
; GENERAL INFORMATION:
;  APPLICANT: Aguinaldo, Anna Marie
;  APPLICANT:  Beyna, Amelia Joy
;  APPLICANT:  Cho, Ho Sung
;  APPLICANT:  Desjarlais, John Rudolph
;  APPLICANT:  Marshall, Shannon Alicia
;  APPLICANT:  Muchhal, Umesh
;  APPLICANT:  Villegas, Michael Francis Aquino
;  APPLICANT:  Zhukovsky, Eugene
;  APPLICANT:  Quesenberry, Michael Stephen
;  TITLE OF INVENTION: INTERFERON VARIANTS WITH IMIPROVED PROPERTIES
;  FILE REFERENCE: A-71431-4
;  CURRENT APPLICATION NUMBER: US/10/820,467
;  CURRENT FILING DATE:  2004-03-30
;  PRIOR APPLICATION NUMBER: US 60/477,246
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: US 60/415,541
;  PRIOR FILING DATE: 2002-10-01
;  PRIOR APPLICATION NUMBER: US 60/489,725
;  PRIOR FILING DATE: 2003-07-24
;  PRIOR APPLICATION NUMBER: US 10/676,705
;  PRIOR FILING DATE: 2003-09-30
;  NUMBER OF SEQ ID NOS: 274
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-820-467-141

  Query Match             32.4%;  Score 34;  DB 5;  Length 9;
  Best Local Similarity   62.5%;  Pred. No. 1.9e+06;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQEF 13
              |||:|:|:
Db          2 HYLKAKEY 9


RESULT 21
```

```
Sequence 61, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:
;  APPLICANT: Ben-Sasson, Shmuel A.
;  TITLE OF INVENTION: Short Peptides Which Selectively
;  TITLE OF INVENTION:  Modulate the Activity of Protein Kinases
;  FILE REFERENCE: 1242.1029-000 (CMCC-679)
;  CURRENT APPLICATION NUMBER: US/10/038,612
;  CURRENT FILING DATE:  2002-01-08
;  PRIOR APPLICATION NUMBER: US 09/161,094
;  PRIOR FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 172
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: unknown
;   FEATURE:
;   OTHER INFORMATION: c-Sea
US-10-038-612-61

  Query Match             30.5%;  Score 32;  DB 4;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 5.5e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQE 12
              |::||||
Db         11 HFIRAQE 17
```

```
Sequence 198, Application US/09755630A
; Publication No. US20030194399A1
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
;  CURRENT APPLICATION NUMBER: US/09/755,630A
;  CURRENT FILING DATE:  2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,669
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 293
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic polypeptide
US-09-755-630A-198

  Query Match             28.6%;  Score 30;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YLRAQE 12
              ||||||
Db          1 YLRAQE 6
```

```
Sequence 198, Application US/10658180
; Publication No. US20040216187A1
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.DVUS02
;  CURRENT APPLICATION NUMBER: US/10/658,180
;  CURRENT FILING DATE:  2003-09-09
;  PRIOR APPLICATION NUMBER: US 09/755,630
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,669
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 295
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic polypeptide
US-10-658-180-198

  Query Match             28.6%;  Score 30;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YLRAQE 12
              ||||||
Db          1 YLRAQE 6
```

```
Sequence 198, Application US/11220856
; Publication No. US20060206962A1
; GENERAL INFORMATION:
;  APPLICANT: ALIBHAI, MURTAZA F.
;  APPLICANT:  ASTWOOD, JAMES D.
;  APPLICANT:  SAMPSON, HUGH A.
;  APPLICANT:  McWHERTER, CHARLES A.
;  TITLE OF INVENTION: PREPARATION OF DEALLERGENIZED PROTEINS AND PERMUTEINS
;  FILE REFERENCE: 11899.0217.DVUS02
;  CURRENT APPLICATION NUMBER: US/11/220,856
;  CURRENT FILING DATE:  2005-09-07
;  PRIOR APPLICATION NUMBER: US/10/658,180
;  PRIOR FILING DATE: 2003-09-09
;  PRIOR APPLICATION NUMBER: US 09/755,630
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,669
;  PRIOR FILING DATE: 2000-01-06
;  NUMBER OF SEQ ID NOS: 295
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic polypeptide
US-11-220-856-198

  Query Match             28.6%;  Score 30;  DB 7;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 75;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 YLRAQE 12
              ||||||
Db          1 YLRAQE 6
```

```
I37261
complement receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I37261
R;Birkenbach, M.; Tong, X.; Bradbury, L.E.; Tedder, T.F.; Kieff, E.
J. Exp. Med. 176, 1405-1414, 1992
A;Title: Characterization of an Epstein-Barr virus receptor on human epithelial cells.
A;Reference number: I37261; MUID:93018869; PMID:1383386
A;Accession: I37261
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-27
A;Cross-references: UNIPROT:Q08578; UNIPARC:UPI0000072008; EMBL:X68990; NID:g3928195;
C;Genetics:
A;Gene: GDB:CR2
A;Cross-references: GDB:119802; OMIM:120650
A;Map position: 1q32-1q32

  Query Match             27.6%;  Score 29;  DB 2;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 HYLRAQ 11
              |||||:
Db          9 HYLRAR 14
```

```
Q4XXI0_PLACH
ID   Q4XXI0_PLACH   PRELIMINARY;   PRT;    25 AA.
AC   Q4XXI0;
DT   05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2005, sequence version 1.
DT   07-FEB-2006, entry version 4.
DE   Hypothetical protein (Fragment).
GN   ORFNames=PC104825.00.0;
OS   Plasmodium chabaudi.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5825;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15637271; DOI=10.1126/science.1103717;
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA   Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA   Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CAAJ01002442; CAH78381.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   25 AA;  2984 MW;  DD02DF108892E750 CRC64;

  Query Match             28.0%;  Score 28;  DB 2;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 6.9e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YVKKVN 7
              |||:||
Db         13 YVKRVN 18
```

```
Q9UCK6_HUMAN
ID   Q9UCK6_HUMAN   PRELIMINARY;   PRT;    19 AA.
AC   Q9UCK6;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 8.
DE   Aspartylglucosaminidase beta 1 subunit (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=93111925; PubMed=1281977;
RA   Rip J.W., Coulter-Mackie M.B., Rupar C.A., Gordon B.A.;
RT   "Purification and structure of human liver aspartylglucosaminidase.";
RL   Biochem. J. 288:1005-1010(1992).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   HSSP; P20933; 1APY.
SQ   SEQUENCE   19 AA;  2127 MW;  BC2F148525610300 CRC64;

  Query Match             27.0%;  Score 27;  DB 2;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 KATEAA 13
              ||||||
Db         13 KATEAA 18
```

```
 Sequence 11, Application US/11136344
; Publication No. US20060178297A1
; GENERAL INFORMATION:
;  APPLICANT: Columbia University
;  APPLICANT:  Troy, Carol M.
;  APPLICANT:  Greene, Lloyd A.
;  TITLE OF INVENTION: SYSTEMS AND METHODS FOR SILENCING
;  TITLE OF INVENTION:  EXPRESSION OF A GENE IN A CELL AND USES THEREOF
;  FILE REFERENCE: 070050.2880
;  CURRENT APPLICATION NUMBER: US/11/136,344
;  CURRENT FILING DATE:  2005-05-23
;  PRIOR APPLICATION NUMBER: US 10/353,902
;  PRIOR FILING DATE: 2003-01-28
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: MPS peptide is a chimera of the hydrophobic
;   OTHER INFORMATION: terminal domain of the viral gp41 protein and the
;   OTHER INFORMATION: nuclear localization signal from simian virus 40
;   OTHER INFORMATION: large antigen.
US-11-136-344-11

  Query Match             34.0%;  Score 34;  DB 7;  Length 27;
  Best Local Similarity   71.4%;  Pred. No. 52;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:||||:
Db          2 ALFLGWL 8
```

```
Sequence 62, Application US/11474283
; Publication No. US20060234308A1
; GENERAL INFORMATION:
;  APPLICANT: Schneider-Mergener, Jens
;  APPLICANT:  Schutkowski, Mike
;  APPLICANT:  Reimer, Ulf
;  APPLICANT:  Dong, Liying
;  APPLICANT:  Panse, Soren
;  APPLICANT:  Scharn, Dirk
;  APPLICANT:  Osterkamp, Frank
;  APPLICANT:  Hummel, Gerd
;  APPLICANT:  Jobron, Laurence
;  TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymati
;  TITLE OF INVENTION:  Activity and a Device Therefor
;  FILE REFERENCE: 2918-0102
;  CURRENT APPLICATION NUMBER: US/11/474,283
;  CURRENT FILING DATE:  2006-06-26
;  PRIOR APPLICATION NUMBER: US/10/475,104
;  PRIOR FILING DATE: 2003-10-17
;  PRIOR APPLICATION NUMBER: PCT/EP02/04265
;  PRIOR FILING DATE: 2002-04-17
;  NUMBER OF SEQ ID NOS: 144
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: synthesized peptide sequence
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (2)..(2)
;   OTHER INFORMATION: Xaa = beta-alanine
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (12)..(12)
;   OTHER INFORMATION: amino group
US-11-474-283-62

  Query Match             25.0%;  Score 25;  DB 7;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 6.8e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 KKVNKATEAA 13
              ||:|:|   |
Db          3 KKLNRALAVA 12
```

```
Sequence 9, Application US/10144549
; Publication No. US20030211590A1
; GENERAL INFORMATION:
;  APPLICANT: GeneShuttle Biopharm, Inc.
;  APPLICANT:  Hwu , Paul  L.
;  TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
;  FILE REFERENCE: MBHB 02-340
;  CURRENT APPLICATION NUMBER: US/10/144,549
;  CURRENT FILING DATE:  2002-05-13
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   OTHER INFORMATION: The fusion sequence of Gp41.
US-10-144-549-9

  Query Match             34.0%;  Score 34;  DB 4;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 2.5e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 AMFLGWV 19
               |:||||:
Db           2 ALFLGWL 8
```

```
Sequence 288, Application US/10226956
; Publication No. US20030060399A1
; GENERAL INFORMATION:
;  APPLICANT: Brophy, Colleen
;  APPLICANT:  Komalavilas, Padmini
;  APPLICANT:  Panitch, Alyssa
;  APPLICANT:  Joshi, Lokesh
;  APPLICANT:  Seal, Brandon L.
;  TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
;  FILE REFERENCE: ASU-1061-US
;  CURRENT APPLICATION NUMBER: US/10/226,956
;  CURRENT FILING DATE:  2002-08-23
;  PRIOR APPLICATION NUMBER: 60/314,535
;  PRIOR FILING DATE: 2001-08-23
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 288
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-10-226-956-288

  Query Match             34.0%;  Score 34;  DB 4;  Length 21;
  Best Local Similarity   71.4%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:|||||:
Db          2 ALFLGWL 8
```

```
Sequence 306, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
;  APPLICANT: Bright, Gary R.
;  APPLICANT:  Premkumar, D. David
;  APPLICANT:  Chen, Yih-Tai
;  TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular
;  FILE REFERENCE: 01-1022-US
;  CURRENT APPLICATION NUMBER: US/10/211,088
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/309,395
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/341,589
;  PRIOR FILING DATE: 2001-12-13
;  NUMBER OF SEQ ID NOS: 366
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 306
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Protein-derived transport peptide
US-10-211-088-306

  Query Match             34.0%;  Score 34;  DB 4;  Length 21;
  Best Local Similarity   71.4%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:|||||:
Db          2 ALFLGWL 8
```

```
Sequence 8, Application US/09785802A
; Patent No. US20020151004A1
; GENERAL INFORMATION:
;  APPLICANT: Craig, Roger
;  TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME
;  FILE REFERENCE: 11067/2035
;  CURRENT APPLICATION NUMBER: US/09/785,802A
;  CURRENT FILING DATE:  2001-02-16
;  PRIOR APPLICATION NUMBER: US 09/748,06
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/748,789
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
US-09-785-802A-8

  Query Match             34.0%;  Score 34;  DB 3;  Length 27;
  Best Local Similarity   71.4%;  Pred. No. 4.1e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:||||:
Db          2 ALFLGWL 8
```

```
Sequence 9, Application US/10144549
; Patent No. 6835810
; GENERAL INFORMATION:
;  APPLICANT: GeneShuttle Biopharm, Inc.
;  APPLICANT:  Hwu , Paul  L.
;  TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
;  FILE REFERENCE: MBHB 02-340
;  CURRENT APPLICATION NUMBER: US/10/144,549
;  CURRENT FILING DATE:  2002-05-13
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Human immunodeficiency virus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   OTHER INFORMATION: The fusion sequence of Gp41.
US-10-144-549-9

  Query Match             34.0%;  Score 34;  DB 2;  Length 17;
  Best Local Similarity   71.4%;  Pred. No. 51;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AMFLGWV 19
              |:|||||:
Db          2 ALFLGWL 8
```

```
 Sequence 73, Application US/10715810
; Publication No. US20050106182A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Shengwen
;  APPLICANT:  Kei, Aoki R.
;  TITLE OF INVENTION: Rescue Agents for Treating a Botulinum Toxin Intoxication
;  FILE REFERENCE: ALLE0004-100
;  CURRENT APPLICATION NUMBER: US/10/715,810
;  CURRENT FILING DATE:  2003-11-17
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Peptide fragment (residues 597-626)
US-10-715-810-73

  Query Match             58.0%;  Score 58;  DB 5;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 ATEAAMFLGWV 19
              ||||||||||
Db          1 ATEAAMFLGWV 11
```

ADG28008
ID ADG28008 standard; peptide; 17 AA.
XX
AC ADG28008;
XX
DT 26-FEB-2004 (first entry)
XX
DE HIV1 gp41 membrane fusion sequence seq id 9.
XX
KW fusion protein; cold shock domain; membrane translocation sequence; CspA;
KW CspB; CspC; CspD; rp1 S1 binding domain; eukaryotic Y-box protein;
KW DNA binding protein B; DBPB; DBPA; EFE-1; mRNP3; mRNP4; FRG Y1;
KW nuclease-sensitive element binding protein 1; NSEP 1;
KW DNA condensation domain; DNA binding domain; SPKR;
KW nuclear localisation sequence; NLS; protein purification tagged sequence;
KW gene delivery; HIV1; gp41; membrane fusion sequence.
XX
OS Human immunodeficiency virus 1.
XX
PN US2003211590-A1.
XX
PD 13-NOV-2003.
XX
PF 13-MAY-2002; 2002US-00144549.
XX
PR 13-MAY-2002; 2002US-00144549.
XX
PA (HWUP/) HWU P L.
XX
PI Hwu PL;
XX
DR WPI; 2003-901590/82.
XX
PT New fusion protein comprising a cold shock domain, and a membrane
PT translocation sequence, useful for delivering DNAs and RNAs to in vivo
PT cells for gene delivery.
XX
PS Claim 9; SEQ ID NO 9; 24pp; English.
XX
CC The invention describes a fusion protein for delivery of a desired
CC molecule into cells or nuclei, comprising a cold shock domain, its
CC homologue and functional derivative, and a membrane translocation
CC sequence or its functional equivalent peptides and/or derivatives. The
CC fusion protein comprises a cold shock domain that is selected from CspA,
CC CspB, CspC, CspD, rp1 S1 binding domain, eukaryotic Y-box proteins, DNA
CC binding protein B (DBPB), DBPA, EFE-1, mRNP3, mRNP4, FRG Y1 and nuclease-
CC sensitive element binding protein 1 (NSEP 1). The functional equivalent
CC derivative of cold shock protein is modified by inserting into the cold
CC shock domain with a DNA condensation domain or a DNA binding domain. The
CC DNA condensation or binding domain is selected from DNA condensation
CC domain (SPKR) 3-4 and the positive charge nuclear localisation sequences
CC (NLS+). The membrane transduction sequence is protein transduction domain
CC (PTD) or membrane fusion sequence. The fusion protein further comprises a
CC protein purification tagged sequence selected from HA, GST, and His6 tag.
CC The fusion protein is useful for delivering DNAs and RNAs to in vivo
CC cells for gene delivery, or for delivering nucleic acids to an embryo or
CC to a living animal for the production of transgenic animal. This is the
CC amino acid sequence of HIV1 gp41 membrane fusion sequence.
XX
SQ Sequence 17 AA;

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  Query Match             34.0%;  Score 34;  DB 7;  Length 17;
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Qy         13 AMFLGWV 19
              |:|||||:
Db          2 ALFLGWL 8
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ABB77687
ID   ABB77687 standard; peptide; 27 AA.
XX
AC   ABB77687;
XX
DT   01-JUL-2002  (first entry)
XX
DE   New peptide vector#3.
XX
KW   Intracellular delivery; transfection agent; cancer; infectious disease;
KW   peptide vector.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 7
FT                   /note= "residue may be substituted with Phe"
FT   Misc-difference 23
FT                   /note= "residue may be substituted with Ser"
XX
PN   WO200210201-A2.
XX
PD   07-FEB-2002.
XX
PF   26-JUL-2001; 2001WO-US023406.
XX
PR   31-JUL-2000; 2000US-0221932P.
XX
PA   (ACTI-) ACTIVE MOTIF.
PA   (CNRS ) CENT NAT RECH SCI.
XX
PI   Divida G,  Morris M,  Mery J,  Heitz F,  Fernandez J,  Archdeacon J;
PI   Horndorp K;
XX
DR   WPI; 2002-329441/36.
XX
PT   Transfection agent that comprises a peptide comprising hydrophobic and
PT   hydrophilic domain and having amino acid residues of specified length is
PT   useful for a non-covalent association with and transport of a
PT   heterologous compound into a cell.
XX
PS   Example 2; Page 61; 156pp; English.
XX
CC   The invention relates to a transfection agent comprises a peptide of
CC   about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC   hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC   between the domains and a functional group conjugated to at least one
CC   terminal of the peptide. Peptides of the invention are useful for a non-
CC   covalent association with and transport of a heterologous compound into a
CC   cell. They are also useful for promoting the cellular internalisation of
CC   at least one member e.g. peptide, proteins, antibodies, their derivatives
CC   and/or conjugates. They may form part of a pharmaceutical composition to
CC   deliver the compound selected from a diagnostic or therapeutic compound,
CC   to treat at least one condition such as cancer or an infectious disease,
CC   or which targets a cancerous cell or pathogen-infected cell and to
CC   deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC   The agent of the invention has a transfection efficiency of at least 5%
CC   for at least two of the members of the group of the compounds. The agent
CC   has a good delivery efficiency for a broad spectrum of compounds and cell
CC   types, has a low toxicity, are easy to handle and easy to formulate in
CC   conjunction with the many different compound types that it can deliver.
```

CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents a
CC new amphipathic peptide vector of the invention that contains a cationic
CC nuclear localisation sequence
XX
SQ Sequence 27 AA;

Query Match 34.0%; Score 34; DB 5; Length 27;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy         13 AMFLGWV 19
              |:||||:
Db          2 ALFLGWL 8
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Q9S937_BETVU
ID   Q9S937_BETVU   PRELIMINARY;   PRT;    24 AA.
AC   Q9S937;
DT   01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT   01-MAY-2000, sequence version 1.
DT   07-FEB-2006, entry version 15.
DE   H(+)-translocating (Pyrophosphate-ENERGIZED) inorganic pyrophosphatase
DE   beta-1 polypeptide (EC 3.6.1.1) (Fragment).
OS   Beta vulgaris (Sugar beet).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   Caryophyllales; Amaranthaceae; Beta.
OX   NCBI_TaxID=161934;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=92179265; PubMed=1311852;
RA   Sarafian V., Kim Y., Poole R.J., Rea P.A.;
RT   "Molecular cloning and sequence of cDNA encoding the pyrophosphate-
RT   energized vacuolar membrane proton pump of Arabidopsis thaliana.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1775-1779(1992).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   PIR; C38230; C38230.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0009678; F:hydrogen-translocating pyrophosphatase acti. . .; IEA.
DR   GO; GO:0004427; F:inorganic diphosphatase activity; IEA.
DR   GO; GO:0015992; P:proton transport; IEA.
DR   InterPro; IPR004131; H_PPase.
DR   Pfam; PF03030; H_PPase; 1.
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Db         17 GPSLNI 22
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Sequence 4, Application US/11249692
; Publication No. US20060148009A1
; GENERAL INFORMATION:
;  APPLICANT: Barbosa, Maria D.F.S.
;  APPLICANT:  Chirino, Arthur J.
;  TITLE OF INVENTION: PREDICTION AND ASSESSMENT OF IMMUNOGENICITY
;  FILE REFERENCE: 185826/US/3 463077-396
;  CURRENT APPLICATION NUMBER: US/11/249,692
;  CURRENT FILING DATE:  2005-10-12
;  PRIOR APPLICATION NUMBER: US 60/659,586
;  PRIOR FILING DATE: 2005-03-08
;  PRIOR APPLICATION NUMBER: US 60/618,154
;  PRIOR FILING DATE: 2004-10-12
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-11-249-692-4

  Query Match             56.6%;  Score 56;  DB 7;  Length 20;
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  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:|||||||||
Db         10 IVPYIGPALNI 20
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:29:25 ; Search time 84.8 Seconds
(without alignments)
102.442 Million cell updates/sec

Title: US-10-821-669-1_COPY_631_649
Perfect score: 99
Sequence: 1 TIIIPYIGPALNIGNMLYK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
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8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	99	100.0	23	9	ADZ69799	Adz69799 Botulinum
3	56	56.6	14	8	ADJ82841	Adj82841 Tetanus T
4	56	56.6	16	2	AAW05608	Aaw05608 Tetanus t
5	56	56.6	20	3	AAY96457	Aay96457 Tetanus t
6	56	56.6	26	5	AAU10838	Aau10838 Human cyt
7	56	56.6	26	8	ADJ82844	Adj82844 Fusion ep
8	56	56.6	27	5	ABB79188	Abb79188 Human cyt
9	56	56.6	28	5	ABB79185	Abb79185 Human cyt
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66	32	32.3	16	8	ADQ90450	Adq90450 RANTES re
67	32	32.3	20	6	ABJ19218	Abj19218 T helper
68	32	32.3	20	7	ADD18054	Add18054 Human G-p
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118	31	31.3	26	3	AAB45058	Aab45058 Human sec
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123	30	30.3	12	2	AAY08852	Aay08852 Expressio
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125	30	30.3	12	4	ABP21702	Abp21702 HIV A03 m
126	30	30.3	14	4	AAM98806	Aam98806 Human pep
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196	29	29.3	21	7	ADF71083	Adf71083 Saccharom
197	29	29.3	23	2	AAY05903	Aay05903 Vicia sat
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200	29	29.3	23	9	ADZ59268	Adz59268 Bidentate
201	29	29.3	23	9	ADZ59266	Adz59266 Bidentate
202	29	29.3	23	9	ADZ59269	Adz59269 Bidentate
203	29	29.3	27	7	ABW02103	Abw02103 Human alp
204	29	29.3	27	7	ADK41528	Adk41528 Anti-cell
205	29	29.3	27	8	ADK50736	Adk50736 Human car
206	29	29.3	28	10	AEE38996	Aee38996 Human ser
207	29	29.3	29	8	ADK50696	Adk50696 Human car
208	29	29.3	30	2	AAY12057	Aay12057 Human 5'
209	29	29.3	30	4	AAB85337	Aab85337 Human oaf
210	29	29.3	30	8	ADI36992	Adi36992 Putative
211	28.5	28.8	17	2	AAR95159	Aar95159 bcl-x(L)/
212	28.5	28.8	17	5	AAE20720	Aae20720 Human Mls
213	28.5	28.8	17	5	AAE21021	Aae21021 Human Icr
214	28.5	28.8	22	8	ADQ16714	Adq16714 Immunoglo
215	28.5	28.8	22	9	ADV44450	Adv44450 Anti-teta
216	28.5	28.8	22	9	AEB12921	Aeb12921 TPO mimet
217	28.5	28.8	23	8	ADT91704	Adt91704 Human rho
218	28.5	28.8	24	3	AAB18706	Aab18706 Synthetic
219	28.5	28.8	29	5	AAU91196	Aau91196 Human E1-
220	28.5	28.8	29	8	ADI79967	Adi79967 E1-E2 ATP
221	28	28.3	9	4	AAB98583	Aab98583 Human TAD
222	28	28.3	9	4	AAB76244	Aab76244 Influenza
223	28	28.3	9	8	ADR22327	Adr22327 Anti-Hepa
224	28	28.3	9	8	ADT73407	Adt73407 Human RSV
225	28	28.3	10	2	AAR12386	Aar12386 Claimed o
226	28	28.3	10	4	AAG87277	Aag87277 Saccharom
227	28	28.3	11	10	AEE71200	Aee71200 Human RCC
228	28	28.3	12	2	AAW10292	Aaw10292 Antiphosp
229	28	28.3	13	2	AAW51834	Aaw51834 Rana temp
230	28	28.3	13	2	AAY50212	Aay50212 Neutrophi
231	28	28.3	13	3	AAB18743	Aab18743 Amino aci
232	28	28.3	14	2	AAR33240	Aar33240 HIV-MC gp
233	28	28.3	15	5	ABB04322	Abb04322 Human zin
234	28	28.3	15	8	ADI95176	Adi95176 OSPF-rela
235	28	28.3	15	9	ADZ82135	Adz82135 Synthetic
236	28	28.3	15	9	AEB52265	Aeb52265 Mucorpeps
237	28	28.3	16	3	AAY99011	Aay99011 HLA class
238	28	28.3	16	5	ABG32207	Abg32207 Sheep col
239	28	28.3	16	7	ADW33651	Adw33651 HLA bindi
240	28	28.3	16	7	ADW36347	Adw36347 HLA bindi
241	28	28.3	16	7	ADW34884	Adw34884 HLA bindi
242	28	28.3	18	10	AEF71020	Aef71020 Human int
243	28	28.3	19	2	AAW98887	Aaw98887 Peptide S
244	28	28.3	19	8	ADK50723	Adk50723 Human car
245	28	28.3	19	8	ADS74417	Ads74417 Ovine col
246	28	28.3	20	1	AAP30113	Aap30113 Sequence
247	28	28.3	20	1	AAP30120	Aap30120 Sequence
248	28	28.3	20	1	AAP30119	Aap30119 Sequence
249	28	28.3	20	1	AAP30118	Aap30118 Sequence
250	28	28.3	20	1	AAP30321	Aap30321 Sequence
251	28	28.3	20	1	AAP30121	Aap30121 Sequence
252	28	28.3	20	1	AAP30320	Aap30320 Sequence
253	28	28.3	20	1	AAP30010	Aap30010 Sequence
254	28	28.3	20	2	AAW82502	Aaw82502 Rabbit OG
255	28	28.3	20	5	ABG75518	Abg75518 HIV-1 p24
256	28	28.3	20	7	ADC99540	Adc99540 Cancer-re

257	28	28.3	20	7	ADC99578	Adc99578 Cancer-re
258	28	28.3	20	7	ADH37199	Adh37199 Human lun
259	28	28.3	20	8	ABM79596	Abm79596 M smegmat
260	28	28.3	20	8	ADN37727	Adn37727 Human imm
261	28	28.3	20	8	ADI95349	Adi95349 OSPF-rela
262	28	28.3	20	8	ADI95350	Adi95350 OSPF-rela
263	28	28.3	20	8	ADI95351	Adi95351 OSPF-rela
264	28	28.3	20	9	ADU98694	Adu98694 Lung tumo
265	28	28.3	20	9	ADW98643	Adw98643 HIV-1 str
266	28	28.3	20	9	ADW95664	Adw95664 HIV-1 gro
267	28	28.3	20	9	ADY59301	Ady59301 HIV-1 p24
268	28	28.3	20	9	ADY59913	Ady59913 HIV-1 p24
269	28	28.3	20	9	ADY59922	Ady59922 HIV-1 gro
270	28	28.3	20	9	ADY71474	Ady71474 HIV-1 gro
271	28	28.3	20	9	AEB10502	Aeb10502 Cancer re
272	28	28.3	20	9	AEE06356	Aee06356 Human lun
273	28	28.3	23	4	AAU04333	Aau04333 ATP-bindi
274	28	28.3	24	2	AAW02299	Aaw02299 HIV-gag p
275	28	28.3	24	8	ADK49287	Adk49287 Human car
276	28	28.3	24	8	AEE66985	Aee66985 Cancer tr
277	28	28.3	25	2	AAW82527	Aaw82527 HIV-1 p24
278	28	28.3	26	8	ADK52109	Adk52109 Human ato
279	28	28.3	27	4	AAM86432	Aam86432 Human imm
280	28	28.3	29	4	AAM84828	Aam84828 Human imm
281	28	28.3	29	8	ADK50724	Adk50724 Human car
282	27.5	27.8	18	4	AAB68103	Aab68103 Peptide d
283	27.5	27.8	21	8	ADM11870	Adm11870 Random pe
284	27.5	27.8	26	2	AAR14988	Aar14988 Part of e
285	27.5	27.8	28	5	AAU91198	Aau91198 Human E1-
286	27.5	27.8	28	8	ADI79969	Adi79969 E1-E2 ATP
287	27.5	27.8	30	2	AAR37008	Aar37008 8-37 pept
288	27.5	27.8	30	4	AAB91150	Aab91150 Pancreati
289	27.5	27.8	30	4	AAB91161	Aab91161 Pancreati
290	27.5	27.8	30	4	AAB91137	Aab91137 Pancreati
291	27.5	27.8	30	4	AAB91148	Aab91148 Pancreati
292	27.5	27.8	30	7	ADE51620	Ade51620 Amylin pe
293	27	27.3	7	8	ADH56413	Adh56413 Escherich
294	27	27.3	7	8	ADO42120	Ado42120 Filovirus
295	27	27.3	8	8	ADH56416	Adh56416 Escherich
296	27	27.3	8	8	ADH56418	Adh56418 Escherich
297	27	27.3	9	4	AAB47575	Aab47575 Ag85 comp
298	27	27.3	9	8	ADP73819	Adp73819 Loop inse
299	27	27.3	9	8	ADP25454	Adp25454 Plasmodiu
300	27	27.3	9	8	ADT74321	Adt74321 Human RSV
301	27	27.3	9	8	ADT73406	Adt73406 Human RSV
302	27	27.3	9	8	ADT73404	Adt73404 Human RSV
303	27	27.3	10	2	AAY47092	Aay47092 Immunogen
304	27	27.3	10	3	ABP41014	Abp41014 Human HER
305	27	27.3	10	3	ABP41032	Abp41032 Human HER
306	27	27.3	10	5	ABG98942	Abg98942 F protein
307	27	27.3	10	5	ABG98943	Abg98943 F protein
308	27	27.3	10	5	ABG98941	Abg98941 F protein
309	27	27.3	10	5	AAU82839	Aau82839 Human Cal
310	27	27.3	10	9	ADW86248	Adw86248 Human cal
311	27	27.3	10	9	ADZ88973	Adz88973 Human cal
312	27	27.3	11	2	AAR63427	Aar63427 Peptide f
313	27	27.3	11	2	AAW27100	Aaw27100 Angiotens
314	27	27.3	11	4	ABP23576	Abp23576 HIV A11 m
315	27	27.3	12	2	AAW31289	Aaw31289 Bovine be
316	27	27.3	12	2	AAW31290	Aaw31290 Bovine be
317	27	27.3	12	6	AAO26477	Aao26477 Debaryomy

318	27	27.3	12	7	ADE41087	Ade41087 Human Apo
319	27	27.3	13	2	AAR46640	Aar46640 65 kD end
320	27	27.3	13	5	AAE27409	Aae27409 Human gra
321	27	27.3	13	5	ADG66715	Adg66715 Human CLC
322	27	27.3	13	5	ADG66717	Adg66717 Human CLC
323	27	27.3	13	5	ADG66716	Adg66716 Human CLC
324	27	27.3	13	5	ADG65764	Adg65764 Human G-C
325	27	27.3	13	6	AAE30632	Aae30632 Human gra
326	27	27.3	13	7	ADJ62461	Adj62461 Tryptic s
327	27	27.3	13	9	AEC11539	Aec11539 Enterococ
328	27	27.3	14	2	AAR60917	Aar60917 TSST-1 am
329	27	27.3	15	2	AAW75679	Aaw75679 M. tuberc
330	27	27.3	15	4	AAB99900	Aab99900 Human fib
331	27	27.3	15	4	ABP24934	Abp24934 HIV DR 3a
332	27	27.3	15	4	ABP24672	Abp24672 HIV DR su
333	27	27.3	15	8	ADU64294	Adu64294 32 KD pro
334	27	27.3	15	9	ADV22459	Adv22459 HIV-1 Pol
335	27	27.3	15	9	ADV23616	Adv23616 HBV immun
336	27	27.3	15	9	ADV23617	Adv23617 HBV immun
337	27	27.3	15	9	ADV22458	Adv22458 HIV-1 Pol
338	27	27.3	15	9	ADZ07230	Adz07230 Hepatitis
339	27	27.3	15	9	AEC13981	Aec13981 E. faecal
340	27	27.3	16	7	ADF92403	Adf92403 Human ubi
341	27	27.3	16	9	ADW98372	Adw98372 Alpha2 53
342	27	27.3	16	9	ADW98447	Adw98447 Alpha2 53
343	27	27.3	17	3	AAB44353	Aab44353 Human sec
344	27	27.3	17	10	AEG01060	Aeg01060 Kallikrei
345	27	27.3	17	10	AEG02788	Aeg02788 Anti-ghre
346	27	27.3	18	9	ADW97883	Adw97883 Hepatitis
347	27	27.3	18	9	AEB77708	Aeb77708 Casomorph
348	27	27.3	19	2	AAR11247	Aar11247 Ala(-2)-G
349	27	27.3	19	5	AAU99837	Aau99837 Human cat
350	27	27.3	19	8	ADR05591	Adr05591 Novel ssD
351	27	27.3	19	8	ADK49226	Adk49226 Human car
352	27	27.3	19	8	ADK50650	Adk50650 Human car
353	27	27.3	19	9	ADW11055	Adw11055 Clostridi
354	27	27.3	19	9	AEC91525	Aec91525 IFN-gamma
355	27	27.3	20	2	AAR74662	Aar74662 Pseudomon
356	27	27.3	20	5	AAE25787	Aae25787 Aspergill
357	27	27.3	20	5	ABB04309	Abb04309 Human PGI
358	27	27.3	20	9	ADW52403	Adw52403 Human PL
359	27	27.3	21	7	ADM56162	Adm56162 C. tracho
360	27	27.3	21	8	ADQ76682	Adq76682 Aprotinin
361	27	27.3	22	3	AAB53228	Aab53228 Protein c
362	27	27.3	22	4	AAM18517	Aam18517 Peptide #
363	27	27.3	22	4	ABB32293	Abb32293 Peptide #
364	27	27.3	22	8	ADH76534	Adh76534 Human neu
365	27	27.3	22	8	ADS33810	Ads33810 cMET-HGF
366	27	27.3	22	8	AEE67082	Aee67082 Cancer tr
367	27	27.3	23	4	AAB50161	Aab50161 Human bra
368	27	27.3	23	4	AAB48158	Aab48158 Human MCH
369	27	27.3	24	2	AAR36998	Aar36998 Amylin an
370	27	27.3	24	2	AAR36999	Aar36999 Ac-24Ser,
371	27	27.3	24	2	AAR37000	Aar37000 Adamantyl
372	27	27.3	24	2	AAY49524	Aay49524 HIV resis
373	27	27.3	24	3	AAB01926	Aab01926 Drosophil
374	27	27.3	24	6	ABG74323	Abg74323 Fruitfly
375	27	27.3	24	9	AEB95963	Aeb95963 Human MCH
376	27	27.3	25	2	AAR36997	Aar36997 Amylin an
377	27	27.3	25	2	AAR68758	Aar68758 Cytotoxic
378	27	27.3	25	2	AAW32895	Aaw32895 HIV pol p

379	27	27.3	25	3	AAB13242	Aab13242 Ascoris s
380	27	27.3	25	4	AAM21747	Aam21747 Peptide #
381	27	27.3	25	4	ABB44116	Abb44116 Peptide #
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383	27	27.3	25	4	ABB27003	Abb27003 Protein #
384	27	27.3	25	4	AAM77843	Aam77843 Human bon
385	27	27.3	25	4	AAM65136	Aam65136 Human bra
386	27	27.3	25	4	ABG59498	Abg59498 Human liv
387	27	27.3	25	4	ABG24168	Abg24168 Novel hum
388	27	27.3	25	5	ABG46871	Abg46871 Human pep
389	27	27.3	25	5	ABG62245	Abg62245 Eubacteri
390	27	27.3	25	5	ABG68684	Abg68684 HIV-1 P21
391	27	27.3	25	7	ADB47951	Adb47951 Novel hum
392	27	27.3	25	7	ADC99605	Adc99605 Cancer-re
393	27	27.3	25	8	ADJ55506	Adj55506 Novel hum
394	27	27.3	25	9	AED67489	Aed67489 Human pep
395	27	27.3	25	10	AEE38542	Aee38542 Human ser
396	27	27.3	25	10	AEF64293	Aef64293 Salmon lo
397	27	27.3	26	2	AAY36392	Aay36392 Fragment
398	27	27.3	26	3	AAY87534	Aay87534 Mature co
399	27	27.3	26	5	AAU81826	Aau81826 Phosphino
400	27	27.3	26	6	ADA11851	Ada11851 Human nov
401	27	27.3	26	8	ADP86220	Adp86220 P2Y2 or P
402	27	27.3	27	2	AAR58337	Aar58337 Hypotensi
403	27	27.3	27	8	ADG37022	Adg37022 Bovine ca
404	27	27.3	28	1	AAP91574	Aap91574 Sequence
405	27	27.3	28	2	AAW57151	Aaw57151 Measles v
406	27	27.3	28	2	AAW57166	Aaw57166 Measles v
407	27	27.3	29	2	AAW78272	Aaw78272 Fragment
408	27	27.3	29	3	AAY91260	Aay91260 Modified
409	27	27.3	29	4	AAM19736	Aam19736 Peptide #
410	27	27.3	29	4	ABB39481	Abb39481 Peptide #
411	27	27.3	29	4	AAM33018	Aam33018 Peptide #
412	27	27.3	29	4	ABB24240	Abb24240 Protein #
413	27	27.3	29	4	AAM72788	Aam72788 Human bon
414	27	27.3	29	4	AAM60171	Aam60171 Human bra
415	27	27.3	29	4	ABG54489	Abg54489 Human liv
416	27	27.3	29	5	ABG42613	Abg42613 Human pep
417	27	27.3	29	8	ADL97675	Adl97675 Protein e
418	27	27.3	29	8	ADK49227	Adk49227 Human car
419	27	27.3	29	8	ADK50651	Adk50651 Human car
420	27	27.3	30	2	AAY39507	Aay39507 HCV E2 pr
421	27	27.3	30	2	AAY14184	Aay14184 HCV envel
422	27	27.3	30	5	ABJ10342	Abj10342 Human lun
423	27	27.3	30	5	AAU84454	Aau84454 HIV POL s
424	27	27.3	30	5	AAU84453	Aau84453 HIV POL s
425	27	27.3	30	8	ADT39600	Adt39600 hSARS vir
426	27	27.3	30	8	ADS79019	Ads79019 SARS viru
427	27	27.3	30	8	ADT37130	Adt37130 hSARS vir
428	27	27.3	30	9	AEA22177	Aea22177 Campyloba
429	26.5	26.8	10	2	AAR53621	Aar53621 Opioid pe
430	26.5	26.8	10	2	AAR89234	Aar89234 SC clone
431	26.5	26.8	18	8	ADK50707	Adk50707 Human car
432	26.5	26.8	20	6	ABP72139	Abp72139 Bombina m
433	26.5	26.8	22	2	AAW96827	Aaw96827 Nucleic a
434	26.5	26.8	24	3	AAB18711	Aab18711 Synthetic
435	26.5	26.8	24	3	AAB18697	Aab18697 Synthetic
436	26.5	26.8	24	8	ADR84154	Adr84154 S. pyogen
437	26.5	26.8	26	2	AAR14987	Aar14987 Part of e
438	26.5	26.8	27	8	ADK50708	Adk50708 Human car
439	26.5	26.8	27	10	AEE38928	Aee38928 Human ser

440	26.5	26.8	28	2	AAR14961	Aar14961 Part of e
441	26.5	26.8	28	2	AAR14974	Aar14974 Part of e
442	26.5	26.8	29	5	AAU91200	Aau91200 Human E1-
443	26.5	26.8	29	5	AAU91199	Aau91199 Human E1-
444	26.5	26.8	29	8	ADI79971	Adi79971 E1-E2 ATP
445	26.5	26.8	29	8	ADI79970	Adi79970 E1-E2 ATP
446	26	26.3	5	6	ABU12136	Abu12136 Bovine BP
447	26	26.3	7	4	AAB49618	Aab49618 HIV-1 int
448	26	26.3	7	9	AEC17603	Aec17603 Casein pe
449	26	26.3	7	9	AEC17851	Aec17851 Casein pe
450	26	26.3	8	2	AAR25090	Aar25090 bGRF prod
451	26	26.3	8	2	AAR25088	Aar25088 bGRF prod
452	26	26.3	8	4	AAB82743	Aab82743 Peptide c
453	26	26.3	8	8	ADK38411	Adk38411 Hepatitis
454	26	26.3	8	9	ADZ05801	Adz05801 Hepatitis
455	26	26.3	8	9	AEC17623	Aec17623 Casein pe
456	26	26.3	8	9	AEC17622	Aec17622 Casein pe
457	26	26.3	8	9	AEC17863	Aec17863 Casein pe
458	26	26.3	8	9	AEC17864	Aec17864 Casein pe
459	26	26.3	9	2	AAR59233	Aar59233 Peptide f
460	26	26.3	9	2	AAR53607	Aar53607 Opioid pe
461	26	26.3	9	2	AAR70067	Aar70067 Control p
462	26	26.3	9	2	AAW54515	Aaw54515 Synthetic
463	26	26.3	9	4	AAE11834	Aae11834 Mycobacte
464	26	26.3	9	5	ABJ07523	Abj07523 Hepatitis
465	26	26.3	9	5	ABJ08794	Abj08794 Hepatitis
466	26	26.3	9	5	ABJ06013	Abj06013 Hepatitis
467	26	26.3	9	5	ABJ09086	Abj09086 Hepatitis
468	26	26.3	9	6	ADA51191	Ada51191 Rous sarc
469	26	26.3	9	7	ABW00526	Abw00526 Human cyt
470	26	26.3	9	8	ADE98275	Ade98275 Immunogen
471	26	26.3	9	8	ADE97695	Ade97695 Immunogen
472	26	26.3	9	8	ADK38662	Adk38662 Hepatitis
473	26	26.3	9	8	ADK38403	Adk38403 Hepatitis
474	26	26.3	9	8	ADK37320	Adk37320 Hepatitis
475	26	26.3	9	8	ADO01394	Ado01394 Human cyt
476	26	26.3	9	8	ADR22340	Adr22340 Anti-Hepa
477	26	26.3	9	8	ADR22326	Adr22326 Anti-Hepa
478	26	26.3	9	8	ADR22332	Adr22332 Anti-Hepa
479	26	26.3	9	8	ADR11427	Adr11427 Hepatitis
480	26	26.3	9	8	ADT73405	Adt73405 Human RSV
481	26	26.3	9	8	ADT73183	Adt73183 Human RSV
482	26	26.3	9	8	ADT73184	Adt73184 Human RSV
483	26	26.3	9	8	ADT72243	Adt72243 Human RSV
484	26	26.3	9	8	ADT73234	Adt73234 Human RSV
485	26	26.3	9	9	ADZ05793	Adz05793 Hepatitis
486	26	26.3	9	9	ADZ06052	Adz06052 Hepatitis
487	26	26.3	9	9	ADZ04710	Adz04710 Hepatitis
488	26	26.3	9	9	ADZ57115	Adz57115 Cytotoxic
489	26	26.3	9	9	AEC17642	Aec17642 Casein pe
490	26	26.3	9	9	AEC17876	Aec17876 Casein pe
491	26	26.3	9	9	AEC17640	Aec17640 Casein pe
492	26	26.3	9	9	AEC17874	Aec17874 Casein pe
493	26	26.3	9	9	AEC17875	Aec17875 Casein pe
494	26	26.3	9	9	AEC17641	Aec17641 Casein pe
495	26	26.3	10	2	AAR25103	Aar25103 bGRF prod
496	26	26.3	10	2	AAR25091	Aar25091 bGRF prod
497	26	26.3	10	2	AAR57928	Aar57928 Randomly
498	26	26.3	10	2	AAR63343	Aar63343 Peptide f
499	26	26.3	10	2	AAR57875	Aar57875 Viral hea
500	26	26.3	10	2	AAR53608	Aar53608 Opioid pe

501	26	26.3	10	2	AAR53618	Aar53618 Opioid pe
502	26	26.3	10	2	AAR96501	Aar96501 Hepatitis
503	26	26.3	10	2	AAW32216	Aaw32216 Alpha-S2
504	26	26.3	10	3	AAY94204	Aay94204 Human cyt
505	26	26.3	10	4	AAB72516	Aab72516 Colostrin
506	26	26.3	10	4	AAB59326	Aab59326 Ewe colos
507	26	26.3	10	4	AAB72263	Aab72263 Colostrin
508	26	26.3	10	4	AAB72548	Aab72548 Colostrin
509	26	26.3	10	4	AAG78080	Aag78080 PB(III) m
510	26	26.3	10	4	AAB66835	Aab66835 Metal ion
511	26	26.3	10	4	AAE11846	Aae11846 M. tuberc

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Sequence 4, Application US/10603094
; Publication No. US20040101534A1
; GENERAL INFORMATION:
;  APPLICANT: Diamond, Don
;  TITLE OF INVENTION: ADJUVANT-FREE PEPTIDE VACCINE
;  FILE REFERENCE: 1954-410
;  CURRENT APPLICATION NUMBER: US/10/603,094
;  CURRENT FILING DATE:  2003-06-25
;  PRIOR APPLICATION NUMBER: US 60/391088
;  PRIOR FILING DATE: 2002-06-25
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Tetanus
US-10-603-094-4

  Query Match             56.6%;  Score 56;  DB 4;  Length 14;
  Best Local Similarity   90.9%;  Pred. No. 0.05;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:||||||||||
Db          4 IVPYIGPALNI 14
```

```
 Sequence 19, Application US/09984365
; Publication No. US20030224980A1
; GENERAL INFORMATION:
;  APPLICANT: Diamond, Don J
;  TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
;  FILE REFERENCE: 1954-384
;  CURRENT APPLICATION NUMBER: US/09/984,365
;  CURRENT FILING DATE:  2002-03-13
;  PRIOR APPLICATION NUMBER: US 09/692170
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 09/534639
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 09/075257
;  PRIOR FILING DATE: 1998-05-11
;  PRIOR APPLICATION NUMBER: US 09/021298
;  PRIOR FILING DATE: 1998-02-10
;  PRIOR APPLICATION NUMBER: US 08/950064
;  PRIOR FILING DATE: 1997-10-14
;  PRIOR APPLICATION NUMBER: US 08/747488
;  PRIOR FILING DATE: 1996-11-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HCMV vaccine peptide
US-09-984-365-19

  Query Match             56.6%;  Score 56;  DB 3;  Length 26;
  Best Local Similarity   90.9%;  Pred. No. 0.097;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:||||||||||
Db          4 IVPYIGPALNI 14
```

```
 Sequence 7, Application US/10603094
; Publication No. US20040101534A1
; GENERAL INFORMATION:
;  APPLICANT: Diamond, Don
;  TITLE OF INVENTION: ADJUVANT-FREE PEPTIDE VACCINE
;  FILE REFERENCE: 1954-410
;  CURRENT APPLICATION NUMBER: US/10/603,094
;  CURRENT FILING DATE:  2003-06-25
;  PRIOR APPLICATION NUMBER: US 60/391088
;  PRIOR FILING DATE: 2002-06-25
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: KTet639V fusion peptide
US-10-603-094-7

  Query Match             56.6%;  Score 56;  DB 4;  Length 26;
  Best Local Similarity   90.9%;  Pred. No. 0.097;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:|||||||||
Db          4 IVPYIGPALNI 14
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```
Sequence 44, Application US/08446692
; Patent No. 5759551
;  GENERAL INFORMATION:
;    APPLICANT:  Ladd, Anna
;    APPLICANT:  Wang, Chang Yi
;    APPLICANT:  Zamb, Timothy
;    TITLE OF INVENTION:  Immunogenic LHRH peptide constructs
;    TITLE OF INVENTION:  and synthetic universal immune stimulators for vaccines
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maria C.H. Lin
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10154-0053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,692
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria C.H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4146 US2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)415-8745
;      TELEFAX:  (516)751-6849
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  16 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-446-692-44

  Query Match             56.6%;  Score 56;  DB 1;  Length 16;
  Best Local Similarity   90.9%;  Pred. No. 0.081;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:|||||||||
Db          5 IVPYIGPALNI 15
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```
Sequence 73, Application PC/TUS9311703
;  GENERAL INFORMATION:
;    APPLICANT:  Chiron Mimotopes Pty. Ltd.
;    TITLE OF INVENTION:  T-Cell Epitopes
;    NUMBER OF SEQUENCES:  75
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Grant D. Green
;      STREET:  4560 Horton St.
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/11703
;      FILING DATE:  28-DEC-1993
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/984,852
;      FILING DATE:  02-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Green, Grant D.
;      REGISTRATION NUMBER:  31,259
;      REFERENCE/DOCKET NUMBER:  0222.101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-601-2706
;      TELEFAX:  510-655-3542
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-11703-73

  Query Match             42.4%;  Score 42;  DB 5;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 5e+05;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPA 10
              |:||||||
Db          1 IVPYIGPA 8
```

```
Sequence 10357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10357
;  LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-10357

  Query Match             30.3%;  Score 30;  DB 2;  Length 30;
  Best Local Similarity   66.7%;  Pred. No. 1e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 IPYIGP 9
              :|:|||
Db         13 VPFIGP 18
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```
Sequence 19, Application US/09984365
; Patent No. 6733973
; GENERAL INFORMATION:
;  APPLICANT: Diamond, Don J
;  TITLE OF INVENTION: IMMUNO-REACTIVE PEPTIDE CTL EPITOPES OF HUMAN CYTOMEGALOVIRUS
;  FILE REFERENCE: 1954-384
;  CURRENT APPLICATION NUMBER: US/09/984,365
;  CURRENT FILING DATE:  2002-03-13
;  PRIOR APPLICATION NUMBER: US 09/692170
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 09/534639
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 09/075257
;  PRIOR FILING DATE: 1998-05-11
;  PRIOR APPLICATION NUMBER: US 09/021298
;  PRIOR FILING DATE: 1998-02-10
;  PRIOR APPLICATION NUMBER: US 08/950064
;  PRIOR FILING DATE: 1997-10-14
;  PRIOR APPLICATION NUMBER: US 08/747488
;  PRIOR FILING DATE: 1996-11-12
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 26
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HCMV vaccine peptide
US-09-984-365-19

  Query Match             56.6%;  Score 56;  DB 2;  Length 26;
  Best Local Similarity   90.9%;  Pred. No. 0.13;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALNI 13
              |:||||||||||
Db          4 IVPYIGPALNI 14
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Sequence 19, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
;  APPLICANT: Chain, Benjamin
;  TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHOD
;  TITLE OF INVENTION:  FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES
;  FILE REFERENCE: 20555/1203433-US1
;  CURRENT APPLICATION NUMBER: US/09/731,899
;  CURRENT FILING DATE:  2000-12-08
;  PRIOR APPLICATION NUMBER: 60/169,687
;  PRIOR FILING DATE: 1999-12-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Tetanus toxin bacteria
US-09-731-899-19
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631-699

```
  Query Match             52.5%;  Score 52;  DB 1;  Length 16;
  Best Local Similarity   90.0%;  Pred. No. 0.031;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IIPYIGPALN 12
              |:||||||||
Db          5 IVPYIGPALN 14
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:30:50 ; Search time 99.3 Seconds
(without alignments)
176.992 Million cell updates/sec

Title: US-10-821-669-1_COPY_631_649
Perfect score: 99
Sequence: 1 TIIIPYIGPALNIGNMLYK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 37017

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	37.4	13	1	CRBL_ICASP	P17237 icaria sp.

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: November 1, 2006, 12:48:32 ; Search time 92.5641 Seconds
(without alignments)
93.850 Million cell updates/sec

Title: US-10-821-669-1_COPY_673_691
Perfect score: 91
Sequence: 1 IPVLGTFALVSYIANKVLT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 1079608

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	91	100.0	19	9	ADW11057	Adw11057 Clostridi
2	91	100.0	27	9	ADW11111	Adw11111 Clostridi
3	44	48.4	27	9	ADW11110	Adw11110 Clostridi
4	43	47.3	27	9	ADW11112	Adw11112 Clostridi
5	34	37.4	16	9	AEB21004	Aeb21004 Aspartate
6	34	37.4	16	9	AEB21006	Aeb21006 Aspartate
7	34	37.4	21	9	AEB21007	Aeb21007 Aspartate
8	34	37.4	21	9	AEB21005	Aeb21005 Aspartate
9	34	37.4	28	8	ABO54884	Abo54884 Human gen
10	33	36.3	21	2	AAY17917	Aay17917 Vesicle t
11	32	35.2	15	2	AAR13976	Aar13976 [Phe14]Me
12	32	35.2	15	2	AAR61467	Aar61467 [Phe- or

13	32	35.2	20	9	ADZ98557	Adz98557 Human ami
14	32	35.2	20	9	ADZ98558	Adz98558 Human ami
15	32	35.2	27	5	ABB89007	Abb89007 Babesia m
16	32	35.2	27	7	ADE06135	Ade06135 BMNI-rela
17	32	35.2	30	10	AEE38707	Aee38707 Human ser
18	31	34.1	10	6	ABR05207	Abr05207 Human can
19	31	34.1	15	6	ABR31075	Abr31075 Human can
20	31	34.1	15	6	ABR30903	Abr30903 Human can
21	31	34.1	15	6	ABR30578	Abr30578 Human can
22	31	34.1	15	6	ABR31050	Abr31050 Human can
23	31	34.1	15	6	ABR31300	Abr31300 Human can
24	31	34.1	15	6	ABR30718	Abr30718 Human can
25	31	34.1	15	6	ABR31535	Abr31535 Human can
26	31	34.1	15	6	ABR30976	Abr30976 Human can
27	31	34.1	15	6	ABR31454	Abr31454 Human can
28	31	34.1	15	6	ABR31586	Abr31586 Human can
29	31	34.1	15	6	ABR31076	Abr31076 Human can
30	31	34.1	15	7	ADE00896	Ade00896 Human 193
31	31	34.1	15	7	ADE00705	Ade00705 Human 193
32	31	34.1	15	7	ADE01050	Ade01050 Human 193
33	31	34.1	15	8	ADP53847	Adp53847 Human 193
34	31	34.1	15	8	ADP53502	Adp53502 Human 193
35	31	34.1	15	8	ADP53693	Adp53693 Human 193
36	31	34.1	15	9	AEB87609	Aeb87609 Brain iso
37	31	34.1	16	7	ABM74151	Abm74151 DNA clone
38	31	34.1	19	2	AAY42677	Aay42677 HHV-6 var
39	31	34.1	21	9	AEB21013	Aeb21013 Aspartate
40	31	34.1	26	2	AAR27267	Aar27267 Signal pe
41	31	34.1	28	10	AEE36906	Aee36906 Human ser
42	30	33.0	10	8	ADK08573	Adk08573 Human pap
43	30	33.0	10	8	ADK08574	Adk08574 Human pap
44	30	33.0	13	9	ADX17310	Adx17310 Human ser
45	30	33.0	15	2	AAR13129	Aar13129 GPIb alph
46	30	33.0	15	2	AAY55128	Aay55128 ATCC HB 1
47	30	33.0	15	3	AAY86874	Aay86874 Human hae
48	30	33.0	15	9	AEB25836	Aeb25836 Peptide O
49	30	33.0	17	2	AAR90401	Aar90401 Antibody
50	30	33.0	17	8	ADS13418	Ads13418 Human rhe
51	30	33.0	19	10	AEE39244	Aee39244 Human ser
52	30	33.0	20	6	ABP83127	Abp83127 G protein
53	30	33.0	23	9	ADV57398	Adv57398 G protein
54	30	33.0	23	9	ADV56511	Adv56511 G protein
55	30	33.0	25	2	AAY12585	Aay12585 Human 5'
56	30	33.0	25	4	AAB65845	Aab65845 Murine IN
57	30	33.0	26	2	AAR38829	Aar38829 Melittin
58	30	33.0	27	4	AAE01286	Aae01286 Human gen
59	30	33.0	27	5	AAU80425	Aau80425 Positive
60	30	33.0	27	5	ABG63719	Abg63719 Human alb
61	30	33.0	27	8	ADL76984	Adl76984 Albumin f
62	30	33.0	28	9	ADV91110	Adv91110 Sodium ch
63	30	33.0	28	9	ADX69229	Adx69229 Voltage-g
64	30	33.0	30	9	AEB95955	Aeb95955 Human mel
65	29.5	32.4	19	6	ABU13492	Abu13492 Zona pell
66	29	31.9	10	4	AAG87763	Aag87763 Saccharom
67	29	31.9	10	4	AAG87762	Aag87762 Saccharom
68	29	31.9	11	9	ADV50819	Adv50819 Murine br
69	29	31.9	13	5	AAE27595	Aae27595 Human bet
70	29	31.9	13	5	AAE27594	Aae27594 Human bet
71	29	31.9	13	5	ADG65892	Adg65892 Human bet
72	29	31.9	13	5	ADG65891	Adg65891 Human bet
73	29	31.9	14	4	AAB61493	Aab61493 Peptide e

74	29	31.9	15	10	AEE39065	Aee39065 Human ser
75	29	31.9	19	5	ABG79262	Abg79262 Human K+a
76	29	31.9	20	4	AAE06796	Aae06796 Human NGM
77	29	31.9	20	8	ADI41254	Adi41254 Human HGP
78	29	31.9	20	8	ADI41294	Adi41294 Human HGP
79	29	31.9	20	9	ADW81161	Adw81161 AMPK modu
80	29	31.9	20	9	ADW81192	Adw81192 AMPK modu
81	29	31.9	20	10	AEF14752	Aef14752 Human cho
82	29	31.9	22	5	ABG79256	Abg79256 Human K+a
83	29	31.9	23	8	ADF69697	Adf69697 Human SLC
84	29	31.9	25	2	AAR49445	Aar49445 Immunomod
85	29	31.9	25	2	AAR49587	Aar49587 Sequence
86	29	31.9	25	2	AAW31864	Aaw31864 MHC class
87	29	31.9	25	2	AAY09341	Aay09341 Human pap
88	29	31.9	25	3	AAY70694	Aay70694 Endoplasm
89	29	31.9	25	3	AAB30292	Aab30292 CD4+ T-ce
90	29	31.9	25	4	AAG67288	Aag67288 Amino aci
91	29	31.9	25	4	AAB95956	Aab95956 HLA-DRalp
92	29	31.9	25	4	AAG64714	Aag64714 HPV immun
93	29	31.9	25	4	AAB20205	Aab20205 HLA-DR-al
94	29	31.9	25	4	AAU03561	Aau03561 Hydrophob
95	29	31.9	25	5	AAO17006	Aao17006 HLA-Dralp
96	29	31.9	25	5	ABG68880	Abg68880 Endoplasm
97	29	31.9	25	5	AAE19014	Aae19014 Hydrophob
98	29	31.9	25	5	ABB09908	Abb09908 Radiolabe
99	29	31.9	25	5	ABB75927	Abb75927 Endoplasm
100	29	31.9	25	5	ABB08107	Abb08107 MHC class
101	29	31.9	25	6	ABU08975	Abu08975 Human exp
102	29	31.9	25	6	AAE35568	Aae35568 Hydrophob
103	29	31.9	25	6	AAO23269	Aao23269 Hydrophob
104	29	31.9	25	6	ABU63379	Abu63379 Human tPA
105	29	31.9	25	7	ABU10009	Abu10009 Human leu
106	29	31.9	25	7	ADF57571	Adf57571 Human sig
107	29	31.9	25	8	ADM13766	Adm13766 MHC class
108	29	31.9	25	8	ADN59204	Adn59204 HLA-DRalp
109	29	31.9	25	8	ADU47822	Adu47822 HPV strai
110	29	31.9	25	9	ADV99799	Adv99799 Glucanase
111	29	31.9	25	10	AEE64440	Aee64440 Human HLA
112	29	31.9	25	10	AEF53024	Aef53024 Signal pe
113	29	31.9	25	10	AEF24307	Aef24307 Endoplasm
114	29	31.9	26	4	AAB50207	Aab50207 Membrane
115	29	31.9	29	5	ABG79237	Abg79237 Human K+a
116	29	31.9	29	5	ABG68893	Abg68893 Secretion
117	29	31.9	30	2	AAY29969	Aay29969 C. elegan
118	29	31.9	30	2	AAY29968	Aay29968 C. elegan
119	28.5	31.3	18	10	AEF71020	Aef71020 Human int
120	28.5	31.3	27	8	ADM97975	Adm97975 Sesquiter
121	28	30.8	9	6	ABR05322	Abr05322 Human can
122	28	30.8	10	6	ABJ38163	Abj38163 Human cyt
123	28	30.8	15	6	ABR31587	Abr31587 Human can
124	28	30.8	15	7	ADE00690	Ade00690 Human 193
125	28	30.8	15	7	ADE00750	Ade00750 Human 193
126	28	30.8	15	7	ADE00938	Ade00938 Human 193
127	28	30.8	15	7	ADE00976	Ade00976 Human 193
128	28	30.8	15	8	ADP53773	Adp53773 Human 193
129	28	30.8	15	8	ADP53735	Adp53735 Human 193
130	28	30.8	15	8	ADP53487	Adp53487 Human 193
131	28	30.8	15	8	ADP53547	Adp53547 Human 193
132	28	30.8	17	9	AEB45051	Aeb45051 B. bovis
133	28	30.8	19	4	ABB43798	Abb43798 Peptide #
134	28	30.8	19	4	AAM77527	Aam77527 Human bon

135	28	30.8	19	4	AAM64763	Aam64763 Human bra
136	28	30.8	19	4	ABG59171	Abg59171 Human liv
137	28	30.8	20	2	AAR39832	Aar39832 E1 peptid
138	28	30.8	23	2	AAR39881	Aar39881 Lipopepti
139	28	30.8	23	9	AEE02004	Aee02004 TM6 domai
140	28	30.8	23	10	AEF20557	Aef20557 Human ost
141	28	30.8	25	8	ABO57373	Abo57373 Human gen
142	28	30.8	26	4	AAB50221	Aab50221 Membrane
143	28	30.8	26	4	AAB50202	Aab50202 Membrane
144	28	30.8	26	4	AAB50204	Aab50204 Membrane
145	28	30.8	26	4	AAB50219	Aab50219 Membrane
146	28	30.8	26	4	AAB50201	Aab50201 Membrane
147	28	30.8	26	4	AAB50210	Aab50210 Membrane
148	28	30.8	26	4	AAB50217	Aab50217 Membrane
149	28	30.8	26	4	AAB50228	Aab50228 Membrane
150	28	30.8	26	4	AAB50229	Aab50229 Membrane
151	28	30.8	26	8	ADH51590	Adh51590 Bee venom
152	28	30.8	26	8	ADP87497	Adp87497 Antimicro
153	28	30.8	26	8	ADR69294	Adr69294 Apis flor
154	28	30.8	27	4	AAM18092	Aam18092 Peptide #
155	28	30.8	27	4	AAB50213	Aab50213 Membrane
156	28	30.8	27	4	AAB50216	Aab50216 Membrane
157	28	30.8	27	4	AAB50227	Aab50227 Membrane
158	28	30.8	27	4	AAB50223	Aab50223 Membrane
159	28	30.8	27	4	AAB50214	Aab50214 Membrane
160	28	30.8	27	4	AAB50225	Aab50225 Membrane
161	28	30.8	27	4	ABB37128	Abb37128 Peptide #
162	28	30.8	27	4	ABB31889	Abb31889 Peptide #
163	28	30.8	27	4	ABB22439	Abb22439 Protein #
164	28	30.8	27	4	AAM70265	Aam70265 Human bon
165	28	30.8	27	4	AAM57847	Aam57847 Human bra
166	28	30.8	27	4	ABG51963	Abg51963 Human liv
167	28	30.8	27	4	AAM05727	Aam05727 Peptide #
168	28	30.8	27	5	ABG39908	Abg39908 Human pep
169	28	30.8	27	5	AAU90989	Aau90989 Transplan
170	28	30.8	27	9	ADX08367	Adx08367 Melittin
171	28	30.8	28	2	AAR89928	Aar89928 A. cellul
172	28	30.8	28	4	AAB50218	Aab50218 Membrane
173	28	30.8	28	4	AAB50230	Aab50230 Membrane
174	28	30.8	28	8	ADH76878	Adh76878 HGG-M2A p
175	28	30.8	28	9	ADV91068	Adv91068 Human sod
176	28	30.8	28	9	ADV91067	Adv91067 Human sod
177	28	30.8	28	9	ADV91069	Adv91069 Human sod
178	28	30.8	28	9	ADX69186	Adx69186 Voltage-g
179	28	30.8	28	9	ADX69187	Adx69187 Voltage-g
180	28	30.8	28	9	ADX69188	Adx69188 Voltage-g
181	28	30.8	29	3	AAB44873	Aab44873 Human sec
182	28	30.8	29	9	AEB54587	Aeb54587 Mouse pre
183	28	30.8	30	1	AAP98449	Aap98449 Sequence
184	28	30.8	30	2	AAR74252	Aar74252 Chlamydia
185	28	30.8	30	2	AAR91524	Aar91524 Chlamydia
186	28	30.8	30	5	ABG68798	Abg68798 C. tracho
187	27.5	30.2	23	4	AAM21121	Aam21121 Peptide #
188	27.5	30.2	23	4	ABB43437	Abb43437 Peptide #
189	27.5	30.2	23	4	AAM37325	Aam37325 Peptide #
190	27.5	30.2	23	4	ABB26407	Abb26407 Protein #
191	27.5	30.2	23	4	AAM64366	Aam64366 Human bra
192	27.5	30.2	23	4	ABG58814	Abg58814 Human liv
193	27	29.7	10	6	ABR05417	Abr05417 Human can
194	27	29.7	10	8	ADS87097	Ads87097 Human gen
195	27	29.7	12	8	ADP87492	Adp87492 Antimicro

196	27	29.7	12	8	AEB44138	Aeb44138 Biomedica
197	27	29.7	14	2	AAW53471	Aaw53471 P2 predom
198	27	29.7	14	8	ADG71721	Adg71721 Human HGP
199	27	29.7	15	2	AAR89150	Aar89150 CAEV env
200	27	29.7	15	5	AAU10987	Aau10987 Human cel
201	27	29.7	15	5	ABG73581	Abg73581 Human zin
202	27	29.7	15	6	ABR32470	Abr32470 Human can
203	27	29.7	15	6	ABR32545	Abr32545 Human can
204	27	29.7	15	6	ABR32424	Abr32424 Human can
205	27	29.7	15	6	ABR31624	Abr31624 Human can
206	27	29.7	15	6	ABR30390	Abr30390 Human can
207	27	29.7	15	6	ABR30904	Abr30904 Human can
208	27	29.7	15	6	ABR31077	Abr31077 Human can
209	27	29.7	15	6	ABR32330	Abr32330 Human can
210	27	29.7	15	7	ADE01056	Ade01056 Human 193
211	27	29.7	15	7	ADE00824	Ade00824 Human 193
212	27	29.7	15	7	ADE00975	Ade00975 Human 193
213	27	29.7	15	7	ADE00937	Ade00937 Human 193
214	27	29.7	15	7	ADE00728	Ade00728 Human 193
215	27	29.7	15	7	ADJ05378	Adj05378 238P1B2 g
216	27	29.7	15	7	ADJ06118	Adj06118 238P1B2 g
217	27	29.7	15	7	ADJ05727	Adj05727 238P1B2 g
218	27	29.7	15	7	ADJ05820	Adj05820 238P1B2 g
219	27	29.7	15	7	ADJ05460	Adj05460 238P1B2 g
220	27	29.7	15	7	ADJ05775	Adj05775 238P1B2 g
221	27	29.7	15	7	ADJ06061	Adj06061 238P1B2 g
222	27	29.7	15	7	ADJ05908	Adj05908 238P1B2 g
223	27	29.7	15	7	ADJ05404	Adj05404 238P1B2 g
224	27	29.7	15	7	ADJ05620	Adj05620 238P1B2 g
225	27	29.7	15	7	ADJ05867	Adj05867 238P1B2 g
226	27	29.7	15	7	ADJ05377	Adj05377 238P1B2 g
227	27	29.7	15	7	ADJ05621	Adj05621 238P1B2 g
228	27	29.7	15	7	ADJ06215	Adj06215 238P1B2 g
229	27	29.7	15	7	ADJ05967	Adj05967 238P1B2 g
230	27	29.7	15	7	ADJ06183	Adj06183 238P1B2 g
231	27	29.7	15	8	ADN58212	Adn58212 238P1B2 H
232	27	29.7	15	8	ADN58309	Adn58309 238P1B2 H
233	27	29.7	15	8	ADN58061	Adn58061 238P1B2 H
234	27	29.7	15	8	ADN57554	Adn57554 238P1B2 H
235	27	29.7	15	8	ADN57914	Adn57914 238P1B2 H
236	27	29.7	15	8	ADN57821	Adn57821 238P1B2 H
237	27	29.7	15	8	ADN58277	Adn58277 238P1B2 H
238	27	29.7	15	8	ADN57714	Adn57714 238P1B2 H
239	27	29.7	15	8	ADN57961	Adn57961 238P1B2 H
240	27	29.7	15	8	ADN57715	Adn57715 238P1B2 H
241	27	29.7	15	8	ADN58002	Adn58002 238P1B2 H
242	27	29.7	15	8	ADN57472	Adn57472 238P1B2 H
243	27	29.7	15	8	ADN57498	Adn57498 238P1B2 H
244	27	29.7	15	8	ADN57869	Adn57869 238P1B2 H
245	27	29.7	15	8	ADN58155	Adn58155 238P1B2 H
246	27	29.7	15	8	ADN57471	Adn57471 238P1B2 H
247	27	29.7	15	8	ADP53621	Adp53621 Human 193
248	27	29.7	15	8	ADP53772	Adp53772 Human 193
249	27	29.7	15	8	ADP53853	Adp53853 Human 193
250	27	29.7	15	8	ADP53525	Adp53525 Human 193
251	27	29.7	15	8	ADP53734	Adp53734 Human 193
252	27	29.7	15	9	AEB87611	Aeb87611 Brain iso
253	27	29.7	16	8	ADO36463	Ado36463 Intracell
254	27	29.7	17	4	ABB38962	Abb38962 Peptide #
255	27	29.7	17	4	AAM32446	Aam32446 Peptide #
256	27	29.7	17	4	AAM72186	Aam72186 Human bon

257	27	29.7	17	4	AAM59613	Aam59613 Human bra
258	27	29.7	17	4	ABG53872	Abg53872 Human liv
259	27	29.7	17	5	ABG42000	Abg42000 Human pep
260	27	29.7	17	8	ADT39045	Adt39045 hSARS vir
261	27	29.7	17	8	ADS78465	Ads78465 SARS viru
262	27	29.7	17	8	ADT36575	Adt36575 hSARS vir
263	27	29.7	17	8	ABY00078	Aby00078 SARS coro
264	27	29.7	18	2	AAW09486	Aaw09486 Thrombopo
265	27	29.7	18	2	AAW36637	Aaw36637 Thrombopo
266	27	29.7	18	4	AAU25856	Aau25856 Human thr
267	27	29.7	18	9	ADV22869	Adv22869 HCV H77 i
268	27	29.7	19	7	ADF14607	Adf14607 Rheumatoi
269	27	29.7	19	8	ADT39130	Adt39130 hSARS vir
270	27	29.7	19	8	ADS78550	Ads78550 SARS viru
271	27	29.7	19	8	ADT36660	Adt36660 hSARS vir
272	27	29.7	19	8	ABY00163	Aby00163 SARS coro
273	27	29.7	19	8	ABY03338	Aby03338 SARS coro
274	27	29.7	19	9	AEC95996	Aec95996 F. hetero
275	27	29.7	20	2	AAR55359	Aar55359 Conformat
276	27	29.7	20	2	AAY01468	Aay01468 Polypepti
277	27	29.7	20	7	ABO23439	Abo23439 Amino aci
278	27	29.7	20	8	ADR20827	Adr20827 Human sec
279	27	29.7	21	2	AAR72296	Aar72296 Glutamic
280	27	29.7	21	2	AAW34051	Aaw34051 Human MDR
281	27	29.7	21	3	AAY59588	Aay59588 GAD65 fra
282	27	29.7	21	8	ADY81194	Ady81194 Rice gene
283	27	29.7	22	6	ABP99586	Abp99586 Human sec
284	27	29.7	22	6	ABR01068	Abr01068 Human gen
285	27	29.7	23	4	AAM88237	Aam88237 Human imm
286	27	29.7	23	4	AAB64425	Aab64425 Human sec
287	27	29.7	24	2	AAW23485	Aaw23485 Antibacte
288	27	29.7	24	4	AAU04309	Aau04309 ATP-bindi
289	27	29.7	25	2	AAW03632	Aaw03632 G-protein
290	27	29.7	25	2	AAY39442	Aay39442 Human Bur
291	27	29.7	25	2	AAW90171	Aaw90171 Triabin/t
292	27	29.7	25	2	AAW90170	Aaw90170 Triabin/t
293	27	29.7	25	5	ABB82365	Abb82365 M11L prot
294	27	29.7	25	5	AAO21800	Aao21800 Lung-spec
295	27	29.7	25	5	AAU78042	Aau78042 Human Bur
296	27	29.7	25	6	ABJ19229	Abj19229 T helper
297	27	29.7	25	9	ADV26014	Adv26014 Myxoma vi
298	27	29.7	26	2	AAR38837	Aar38837 Melittin
299	27	29.7	26	2	AAR38838	Aar38838 Melittin
300	27	29.7	26	2	AAY30916	Aay30916 Human sec
301	27	29.7	26	8	ADG71689	Adg71689 Human HGP
302	27	29.7	26	10	AEE37498	Aee37498 Human ser
303	27	29.7	27	8	ADK50716	Adk50716 Human car
304	27	29.7	28	3	AAB28711	Aab28711 Human sec
305	27	29.7	28	5	ABG78096	Abg78096 ITALY, LO
306	27	29.7	28	8	ADR45672	Adr45672 Rat G pro
307	27	29.7	28	9	ADV91050	Adv91050 Rat sodiu
308	27	29.7	28	9	ADV91043	Adv91043 Human sod
309	27	29.7	28	9	ADV91049	Adv91049 Rat sodiu
310	27	29.7	28	9	ADV91044	Adv91044 Human sod
311	27	29.7	28	9	ADV91047	Adv91047 Rat sodiu
312	27	29.7	28	9	ADX69166	Adx69166 Voltage-g
313	27	29.7	28	9	ADX69168	Adx69168 Voltage-g
314	27	29.7	28	9	ADX69169	Adx69169 Voltage-g
315	27	29.7	28	9	ADX69162	Adx69162 Voltage-g
316	27	29.7	28	9	ADX69163	Adx69163 Voltage-g
317	27	29.7	29	4	AAB60729	Aab60729 Human sec

318	27	29.7	29	5	AAU98712	Aau98712 Human cyc
319	27	29.7	29	8	ADP87495	Adp87495 Antimicro
320	27	29.7	29	8	ADP87494	Adp87494 Antimicro
321	27	29.7	29	8	AEB44140	Aeb44140 Biomedica
322	27	29.7	29	8	AEB44141	Aeb44141 Biomedica
323	27	29.7	30	1	AAP80653	Aap80653 Peptide e
324	27	29.7	30	2	AAR05809	Aar05809 Signal pe
325	27	29.7	30	2	AAY41529	Aay41529 Fragment
326	27	29.7	30	5	AAU84648	Aau84648 HCV HepC1
327	26.5	29.1	16	9	AEA27278	Aea27278 Stress to
328	26.5	29.1	19	5	AAU99839	Aau99839 Human cat
329	26.5	29.1	25	2	AAR39772	Aar39772 Melittin
330	26.5	29.1	25	2	AAR39770	Aar39770 Melittin
331	26.5	29.1	28	2	AAW40014	Aaw40014 Peptide e
332	26.5	29.1	30	5	ABP29172	Abp29172 Streptoco
333	26	28.6	9	2	AAR51596	Aar51596 Mimotope
334	26	28.6	9	2	AAR69971	Aar69971 Nonameric
335	26	28.6	9	2	AAR98719	Aar98719 Peptide 2
336	26	28.6	9	2	AAY46520	Aay46520 Immunogen
337	26	28.6	9	7	ADW32181	Adw32181 HLA bindi
338	26	28.6	9	7	ADW31315	Adw31315 HLA bindi
339	26	28.6	10	9	ADZ04488	Adz04488 Alpha1-an
340	26	28.6	12	6	ABR42901	Abr42901 Bovine hi
341	26	28.6	12	9	AEB94175	Aeb94175 Serum CD2
342	26	28.6	13	6	ABR59542	Abr59542 S. aureus
343	26	28.6	13	9	AEB94174	Aeb94174 Serum CD2
344	26	28.6	13	9	AED27713	Aed27713 Tyrosyl-t
345	26	28.6	14	2	AAW40030	Aaw40030 Cytoplasm
346	26	28.6	14	4	AAG99376	Aag99376 Proteasom
347	26	28.6	14	4	AAE05991	Aae05991 Peptide #
348	26	28.6	14	7	ADH89139	Adh89139 E. avium
349	26	28.6	15	2	AAR13975	Aar13975 [Leu14]Me
350	26	28.6	15	2	AAR61466	Aar61466 [Leu-14]
351	26	28.6	15	7	ADD24084	Add24084 Breast ca
352	26	28.6	15	7	ADD23632	Add23632 Breast ca
353	26	28.6	15	8	ADL70918	Adl70918 PTP1B pho
354	26	28.6	15	8	ADL70822	Adl70822 PTP1B pho
355	26	28.6	15	8	ADL70917	Adl70917 PTP1B pho
356	26	28.6	15	8	ADP26537	Adp26537 Plasmodiu
357	26	28.6	16	7	ADM47482	Adm47482 Bioactive
358	26	28.6	16	8	ADI41077	Adi41077 Human HGP
359	26	28.6	16	8	ADI41155	Adi41155 Human HGP
360	26	28.6	16	8	ADI41115	Adi41115 Human HGP
361	26	28.6	17	7	ADJ00164	Adj00164 238P1B2 g
362	26	28.6	17	8	ADN52266	Adn52266 238P1B2 H
363	26	28.6	18	3	AAB51856	Aab51856 Human sec
364	26	28.6	18	4	AAG99373	Aag99373 Proteasom
365	26	28.6	18	7	ADG73501	Adg73501 Enterococ
366	26	28.6	18	9	AEC11101	Aec11101 Enterococ
367	26	28.6	18	10	AEE36861	Aee36861 Human ser
368	26	28.6	19	2	AAY16640	Aay16640 WO9914235
369	26	28.6	19	3	AAB28825	Aab28825 Geminivir
370	26	28.6	19	7	ADJ00165	Adj00165 238P1B2 g
371	26	28.6	19	8	ADH89725	Adh89725 Cell pene
372	26	28.6	19	8	ADN52267	Adn52267 238P1B2 H
373	26	28.6	19	9	ADX56727	Adx56727 Cardiovas
374	26	28.6	19	9	ADY38118	Ady38118 Human CPP
375	26	28.6	19	9	ADZ80725	Adz80725 Amino aci
376	26	28.6	19	9	ADZ80726	Adz80726 Amino aci
377	26	28.6	19	9	AED43095	Aed43095 Persephin
378	26	28.6	19	9	AED68502	Aed68502 Membrane-

379	26	28.6	19	9	AED89965	Aed89965 Membrane
380	26	28.6	19	10	AEE25291	Aee25291 Transport
381	26	28.6	19	10	AEF51810	Aef51810 Transport
382	26	28.6	20	2	AAR42715	Aar42715 Guinea pi
383	26	28.6	20	2	AAR42714	Aar42714 Murine TG
384	26	28.6	20	2	AAY40856	Aay40856 Amino aci
385	26	28.6	20	7	ADF28112	Adf28112 Complemen
386	26	28.6	20	7	ADF28102	Adf28102 Complemen
387	26	28.6	20	8	ADH37342	Adh37342 Epstein B
388	26	28.6	20	8	ADH37343	Adh37343 Epstein B
389	26	28.6	20	8	ADU17214	Adu17214 M. tuberc
390	26	28.6	20	9	ADW52238	Adw52238 Human PL
391	26	28.6	20	9	ADZ98147	Adz98147 Human ami
392	26	28.6	20	9	AEE34822	Aee34822 Wheat gli
393	26	28.6	20	9	AEE34823	Aee34823 Wheat gli
394	26	28.6	20	10	AEF09682	Aef09682 Monkeypox
395	26	28.6	21	2	AAW34062	Aaw34062 GPCR anta
396	26	28.6	21	2	AAW26292	Aaw26292 Peptide 6
397	26	28.6	21	2	AAW40031	Aaw40031 Peptide d
398	26	28.6	21	7	ADJ93115	Adj93115 Human G-c
399	26	28.6	21	9	ADY63840	Ady63840 Human apo
400	26	28.6	22	2	AAR70673	Aar70673 Transmemb
401	26	28.6	22	7	ADJ93201	Adj93201 Human G-c
402	26	28.6	22	9	AED68501	Aed68501 Membrane-
403	26	28.6	22	9	AED89964	Aed89964 Membrane
404	26	28.6	22	10	AEE25290	Aee25290 Transport
405	26	28.6	22	10	AEF51809	Aef51809 Transport
406	26	28.6	24	2	AAR66208	Aar66208 N-termina
407	26	28.6	24	2	AAW26284	Aaw26284 Peptide A
408	26	28.6	24	2	AAW26285	Aaw26285 Peptide A
409	26	28.6	25	2	AAR39760	Aar39760 Melittin
410	26	28.6	25	2	AAR39765	Aar39765 Melittin
411	26	28.6	25	2	AAR39763	Aar39763 Melittin
412	26	28.6	25	2	AAR39761	Aar39761 Melittin
413	26	28.6	25	2	AAR39766	Aar39766 Melittin
414	26	28.6	25	2	AAR39768	Aar39768 Melittin
415	26	28.6	25	2	AAR39762	Aar39762 Melittin
416	26	28.6	25	2	AAR39769	Aar39769 Melittin
417	26	28.6	25	2	AAR39783	Aar39783 Melittin
418	26	28.6	25	2	AAR39764	Aar39764 Melittin
419	26	28.6	25	2	AAR39782	Aar39782 Melittin
420	26	28.6	25	2	AAR39767	Aar39767 Melittin
421	26	28.6	25	2	AAM48358	Aam48358 Antifunga
422	26	28.6	25	3	AAY71483	Aay71483 Ehrlichia
423	26	28.6	25	5	AAU96113	Aau96113 Ehrlichia
424	26	28.6	25	7	ADM80761	Adm80761 Melittin
425	26	28.6	25	8	ADH89721	Adh89721 Cell pene
426	26	28.6	25	9	AED68499	Aed68499 Membrane-
427	26	28.6	25	9	AED89962	Aed89962 Membrane
428	26	28.6	25	10	AEE25288	Aee25288 Transport
429	26	28.6	25	10	AEF51807	Aef51807 Transport
430	26	28.6	26	1	AAP91340	Aap91340 Amino aci
431	26	28.6	26	2	AAR13908	Aar13908 Guanidina
432	26	28.6	26	2	AAR22990	Aar22990 Melittin
433	26	28.6	26	2	AAR39788	Aar39788 Melittin
434	26	28.6	26	2	AAR38828	Aar38828 Melittin
435	26	28.6	26	2	AAR39789	Aar39789 Melittin
436	26	28.6	26	2	AAR39759	Aar39759 Melittin
437	26	28.6	26	2	AAR38839	Aar38839 Melittin
438	26	28.6	26	2	AAR38834	Aar38834 Melittin
439	26	28.6	26	2	AAR39784	Aar39784 Melittin

440	26	28.6	26	2	AAR39785	Aar39785 Melittin
441	26	28.6	26	2	AAR38827	Aar38827 Melittin
442	26	28.6	26	2	AAR39790	Aar39790 Melittin
443	26	28.6	26	2	AAR35383	Aar35383 Melittin
444	26	28.6	26	2	AAR45114	Aar45114 Melittin
445	26	28.6	26	2	AAR50565	Aar50565 Amphiphil
446	26	28.6	26	2	AAR55989	Aar55989 Ion chann
447	26	28.6	26	2	AAR59067	Aar59067 Melittin,
448	26	28.6	26	2	AAR56950	Aar56950 Peptide w
449	26	28.6	26	2	AAR50430	Aar50430 Amphiphil
450	26	28.6	26	2	AAR85516	Aar85516 Melittin.
451	26	28.6	26	2	AAR72973	Aar72973 Calmoduli
452	26	28.6	26	2	AAR90136	Aar90136 Melittin
453	26	28.6	26	2	AAW08667	Aaw08667 Honeybee
454	26	28.6	26	2	AAW09134	Aaw09134 Melittin
455	26	28.6	26	2	AAW23502	Aaw23502 Antibacte
456	26	28.6	26	2	AAW16374	Aaw16374 Honeybee
457	26	28.6	26	2	AAW35146	Aaw35146 Melittin-
458	26	28.6	26	2	AAW35145	Aaw35145 Melittin-
459	26	28.6	26	2	AAW77385	Aaw77385 Lytic pep
460	26	28.6	26	2	AAW66453	Aaw66453 Cationic
461	26	28.6	26	2	AAW43128	Aaw43128 Melittin,
462	26	28.6	26	2	AAW71674	Aaw71674 Melittin-
463	26	28.6	26	2	AAW82879	Aaw82879 Antipatho
464	26	28.6	26	2	AAW82880	Aaw82880 Antipatho
465	26	28.6	26	2	AAY22019	Aay22019 Melittin.
466	26	28.6	26	2	AAW87611	Aaw87611 Antimicro
467	26	28.6	26	2	AAW95333	Aaw95333 Synthetic
468	26	28.6	26	2	AAY10732	Aay10732 Peptide u
469	26	28.6	26	3	AAB12439	Aab12439 Plasmid c
470	26	28.6	26	3	AAY44325	Aay44325 Antimicro
471	26	28.6	26	3	AAY91752	Aay91752 Cationic
472	26	28.6	26	3	AAB17408	Aab17408 Antipatho
473	26	28.6	26	3	AAB17407	Aab17407 Antipatho
474	26	28.6	26	3	AAB17409	Aab17409 Antipatho
475	26	28.6	26	3	AAB11034	Aab11034 Apis mell
476	26	28.6	26	4	AAM20092	Aam20092 Peptide #
477	26	28.6	26	4	AAB50205	Aab50205 Membrane
478	26	28.6	26	4	AAB50209	Aab50209 Membrane
479	26	28.6	26	4	AAB50199	Aab50199 Membrane
480	26	28.6	26	4	AAB50200	Aab50200 Membrane
481	26	28.6	26	4	AAB92169	Aab92169 Signal tr
482	26	28.6	26	4	ABB40276	Abb40276 Peptide #
483	26	28.6	26	4	ABB39475	Abb39475 Peptide #
484	26	28.6	26	4	ABB42416	Abb42416 Peptide #
485	26	28.6	26	4	AAM33959	Aam33959 Peptide #
486	26	28.6	26	4	AAM36226	Aam36226 Peptide #
487	26	28.6	26	4	AAM33012	Aam33012 Peptide #
488	26	28.6	26	4	AAG99362	Aag99362 Proteasom
489	26	28.6	26	4	AAB50842	Aab50842 Bee prote
490	26	28.6	26	4	ABB25868	Abb25868 Protein #
491	26	28.6	26	4	ABB24689	Abb24689 Protein #
492	26	28.6	26	4	AAM73772	Aam73772 Human bon
493	26	28.6	26	4	AAM72782	Aam72782 Human bon
494	26	28.6	26	4	AAM76117	Aam76117 Human bon
495	26	28.6	26	4	AAM63301	Aam63301 Human bra
496	26	28.6	26	4	AAM61069	Aam61069 Human bra
497	26	28.6	26	4	AAM60166	Aam60166 Human bra
498	26	28.6	26	4	ABG57838	Abg57838 Human liv
499	26	28.6	26	4	ABG55518	Abg55518 Human liv
500	26	28.6	26	4	ABG54483	Abg54483 Human liv

501	26	28.6	26	4	AAY72458	Aay72458 Mellitin
502	26	28.6	26	5	AAM49738	Aam49738 Peptide f
503	26	28.6	26	5	ABG43657	Abg43657 Human pep
504	26	28.6	26	5	ABG45484	Abg45484 Human pep
505	26	28.6	26	5	ABG42607	Abg42607 Human pep
506	26	28.6	26	5	ABB73012	Abb73012 Antipatho
507	26	28.6	26	5	ABB73010	Abb73010 Antipatho
508	26	28.6	26	5	ABB73011	Abb73011 Antipatho
509	26	28.6	26	5	ABB81941	Abb81941 Peptide f
510	26	28.6	26	5	AAE18196	Aae18196 Apis mell
511	26	28.6	26	5	AAE18198	Aae18198 Procytoto
512	26	28.6	26	5	AAE22445	Aae22445 Biologica
513	26	28.6	26	5	ABB81263	Abb81263 [D]-Melit
514	26	28.6	26	5	ABB81262	Abb81262 Melittin
515	26	28.6	26	5	AAO21742	Aao21742 Melittin
516	26	28.6	26	5	AAO21734	Aao21734 Melittin
517	26	28.6	26	5	AAO21740	Aao21740 Procytoto
518	26	28.6	26	6	ABU07618	Abu07618 Crystal a
519	26	28.6	26	6	ABU59630	Abu59630 Cationic
520	26	28.6	26	6	ABR00830	Abr00830 Bioactive
521	26	28.6	26	7	ADF18363	Adf18363 Antibacte
522	26	28.6	26	7	ADG88568	Adg88568 Crystal a
523	26	28.6	26	7	ADJ73166	Adj73166 Antipatho
524	26	28.6	26	7	ADJ73165	Adj73165 Antipatho
525	26	28.6	26	7	ADJ73164	Adj73164 Antipatho
526	26	28.6	26	8	ADJ52801	Adj52801 CH1 delet
527	26	28.6	26	8	ADJ52800	Adj52800 CH1 delet
528	26	28.6	26	8	ADJ52799	Adj52799 CH1 delet
529	26	28.6	26	8	ADJ51762	Adj51762 CH1 delet
530	26	28.6	26	8	ADJ51760	Adj51760 CH1 delet
531	26	28.6	26	8	ADJ51761	Adj51761 CH1 delet
532	26	28.6	26	8	ADJ78628	Adj78628 Purificat
533	26	28.6	26	8	ADO59380	Ado59380 Melittin
534	26	28.6	26	8	ADP74183	Adp74183 Melittin
535	26	28.6	26	8	ADR12685	Adr12685 Bee melit
536	26	28.6	26	8	ADU69235	Adu69235 Honey bee
537	26	28.6	26	9	ADW73980	Adw73980 Honey bee
538	26	28.6	26	9	ADY67501	Ady67501 Tumor cel
539	26	28.6	26	9	ADZ60124	Adz60124 Melittin
540	26	28.6	26	9	AEA47560	Aea47560 Amino aci
541	26	28.6	26	9	AEC60349	Aec60349 Biodegrad
542	26	28.6	26	9	AEC60348	Aec60348 Biodegrad
543	26	28.6	26	10	AEE36724	Aee36724 Human ser
544	26	28.6	26	10	AEE99045	Aee99045 Tumor tis
545	26	28.6	26	10	AEF61738	Aef61738 Modified
546	26	28.6	26	10	AEF61737	Aef61737 Modified
547	26	28.6	26	10	AEF61736	Aef61736 Modified
548	26	28.6	26	10	AEF69156	Aef69156 ES-HER2/n
549	26	28.6	26	10	AEG07876	Aeg07876 Peptide 2
550	26	28.6	27	2	AAW66392	Aaw66392 Bee venom
551	26	28.6	27	5	ABB81271	Abb81271 Antibacte
552	26	28.6	27	5	ABB81236	Abb81236 Antibacte
553	26	28.6	27	8	ABO56899	Abo56899 Human gen
554	26	28.6	27	8	ADK49194	Adk49194 Human car
555	26	28.6	27	9	ADV60176	Adv60176 COX pepti
556	26	28.6	27	9	AEC32680	Aec32680 Keratinoc
557	26	28.6	28	1	AAP60883	Aap60883 Synthetic
558	26	28.6	28	2	AAY02954	Aay02954 Fragment
559	26	28.6	28	4	AAM13591	Aam13591 Peptide #
560	26	28.6	28	4	ABB32521	Abb32521 Peptide #
561	26	28.6	28	4	AAM25989	Aam25989 Peptide #

562	26	28.6	28	4	AAB85397	Aab85397 Stem cell
563	26	28.6	28	4	ABB27373	Abb27373 Human pep
564	26	28.6	28	4	ABB18026	Abb18026 Protein #
565	26	28.6	28	4	AAM65732	Aam65732 Human bon
566	26	28.6	28	4	AAM53353	Aam53353 Human bra
567	26	28.6	28	4	ABG47373	Abg47373 Human liv
568	26	28.6	28	4	AAM01341	Aam01341 Peptide #
569	26	28.6	28	5	ABG35361	Abg35361 Human pep
570	26	28.6	28	6	ABO01431	Abo01431 Human ste
571	26	28.6	28	6	ABR63692	Abr63692 Human bre
572	26	28.6	28	7	ADA07789	Ada07789 Human sec
573	26	28.6	28	8	ADN41475	Adn41475 Novel hum
574	26	28.6	28	9	ADV91039	Adv91039 Human sod
575	26	28.6	28	9	ADV91041	Adv91041 Human sod
576	26	28.6	28	9	ADV91042	Adv91042 Human sod
577	26	28.6	28	9	ADV91040	Adv91040 Human sod
578	26	28.6	28	9	ADV91045	Adv91045 Human sod
579	26	28.6	28	9	ADV91046	Adv91046 Rat sodiu
580	26	28.6	28	9	ADX69165	Adx69165 Voltage-g
581	26	28.6	28	9	ADX69158	Adx69158 Voltage-g
582	26	28.6	28	9	ADX69160	Adx69160 Voltage-g
583	26	28.6	28	9	ADX69159	Adx69159 Voltage-g
584	26	28.6	28	9	ADX69164	Adx69164 Voltage-g
585	26	28.6	28	9	ADX69161	Adx69161 Voltage-g
586	26	28.6	29	2	AAR09355	Aar09355 Sequence
587	26	28.6	29	3	AAY65201	Aay65201 Human 5'
588	26	28.6	29	7	ADJ00166	Adj00166 238P1B2 g
589	26	28.6	29	8	ADN52268	Adn52268 238P1B2 H
590	26	28.6	29	8	ADU72765	Adu72765 Signal pe
591	26	28.6	29	9	ADZ73756	Adz73756 Human inc
592	26	28.6	30	2	AAR98027	Aar98027 Fusogenic
593	26	28.6	30	3	AAY64891	Aay64891 Human 5'
594	26	28.6	30	4	AAU30169	Aau30169 Novel hum
595	26	28.6	30	5	AAU84956	Aau84956 Human Trp

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Sequence 209, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
;  APPLICANT: Kantor, Aaron B.
;  APPLICANT:  Schulman, Howard
;  APPLICANT:  Becker, Christopher
;  TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
;  FILE REFERENCE: SURR.121
;  CURRENT APPLICATION NUMBER: US/10/801,990
;  CURRENT FILING DATE:  2004-03-15
;  PRIOR APPLICATION NUMBER: US 60/455,037
;  PRIOR FILING DATE: 2003-03-14
;  NUMBER OF SEQ ID NOS: 395
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-801-990-209

  Query Match             33.0%;  Score 30;  DB 5;  Length 17;
  Best Local Similarity   85.7%;  Pred. No. 6.5e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FALVSYI 13
              ||||:||
Db          8 FALVNYI 14
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```
Sequence 10, Application US/09178093B
; Patent No. 6660846
; GENERAL INFORMATION:
;  APPLICANT: Robert H. Edwards
;  APPLICANT:  Richard J. Reimer
;  APPLICANT:  Steve L. McIntire
;  APPLICANT:  Erik M. Jorgenson
;  APPLICANT:  Kim Schuske
;  TITLE OF INVENTION: Vesicular Amino Acid Transported
;  TITLE OF INVENTION:  Composition and Method
;  FILE REFERENCE: 2002-0005.30
;  CURRENT APPLICATION NUMBER: US/09/178,093B
;  CURRENT FILING DATE:  2001-08-20
;  PRIOR APPLICATION NUMBER: 60/063,012
;  PRIOR FILING DATE: 1997-10-23
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 21
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-178-093B-10

  Query Match             36.3%;  Score 33;  DB 2;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GTFALVSYI 13
              | ||||:|:
Db         11 GLFALVAYL 19
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Sequence 33, Application US/07643343A
; Patent No. 5235038
;  GENERAL INFORMATION:
;    APPLICANT:  Blondelle, Sylvie E.
;    APPLICANT:  Houghten, Richard A.
;    TITLE OF INVENTION:  Deletion and Substitution
;    TITLE OF INVENTION:  Analogues of Melittin Peptide
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan,
;      ADDRESSEE:  Cecchi & Stewart
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  DW4.V2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/643,343A
;      FILING DATE:  19910122
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  421250-139
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  substitution analogue of melittin
;      NAME/KEY:  peptide
US-07-643-343A-33

  Query Match             33.0%;  Score 30;  DB 1;  Length 26;
  Best Local Similarity   53.8%;  Pred. No. 1.8e+02;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 LGTFALVSYIANK 16
              ||  ||:|:|  |
Db         11 LGLPALISWIKRK 23
```

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Sequence 42, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
;  GENERAL INFORMATION:
;    APPLICANT:  Dower, William J.
;    APPLICANT:  Barrett, Ronald W.
;    APPLICANT:  Cwirla, Steven E.
;    APPLICANT:  Gates, Christian
;    APPLICANT:  Schatz, Peter J.
;    APPLICANT:  Balasubramanian, Palaniappan
;    APPLICANT:  Wagstrom, Christopher R.
;    APPLICANT:  Hendren, Richard W.
;    APPLICANT:  Deprince, Randolph B.
;    APPLICANT:  Podduturi, Surekha
;    APPLICANT:  Yin, Qun
;    TITLE OF INVENTION:  PEPTIDES AND COMPOUNDS THAT BIND TO A
;    TITLE OF INVENTION:  RECEPTOR
;    NUMBER OF SEQUENCES:  244
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Glaxo Wellcome
;      STREET:  Five Moore Drive, P.O. Box 13398
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/764,640
;      FILING DATE:  11-DEC-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hrubiec, Robert T.
;      REGISTRATION NUMBER:  36,392
;      REFERENCE/DOCKET NUMBER:  PK3281
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-248-1000
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-764-640-42

  Query Match             29.7%;  Score 27;  DB 1;  Length 18;
  Best Local Similarity   62.5%;  Pred. No. 3.9e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LGTFALVS 11
              ||:|:|:|
Db         11 LGSFSLLS 18
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Sequence 42, Application US/09516704
; Patent No. 6251864
;   GENERAL INFORMATION:
;        APPLICANT: Dower, William J.
;                   Barrett, Ronald W.
;                   Cwirla, Steven E.
;                   Gates, Christian
;                   Schatz, Peter J.
;                   Balasubramanian, Palaniappan
;                   Wagstrom, Christopher R.
;                   Hendren, Richard W.
;                   Deprince, Randolph B.
;                   Podduturi, Surekha
;        TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
;                            RECEPTOR
;        NUMBER OF SEQUENCES: 244
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Glaxo Wellcome
;             STREET: Five Moore Drive, P.O. Box 13398
;             CITY: Research Triangle Park
;             STATE: NC
;             COUNTRY: USA
;             ZIP: 27709
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/516,704
;             FILING DATE: 01-Mar-2000
;             CLASSIFICATION:
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hrubiec, Robert T.
;             REGISTRATION NUMBER: 36,392
;             REFERENCE/DOCKET NUMBER: PK3281
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 919-248-1000
;   INFORMATION FOR SEQ ID NO: 42:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 amino acids
;             TYPE: amino acid
;             STRANDEDNESS:
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-516-704-42

  Query Match             29.7%;  Score 27;  DB 2;  Length 18;
  Best Local Similarity   62.5%;  Pred. No. 3.9e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 LGTFALVS 11
              ||:|:|:|
Db         11 LGSFSLLS 18
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AAY17917
ID   AAY17917 standard; peptide; 21 AA.
XX
AC   AAY17917;
XX
DT   02-AUG-1999  (first entry)
XX
DE   Vesicle transporter protein, RUNC-47 transmembrane domain 6.
XX
KW   Vesicle transporter protein; synaptic vesicle; UNC-47; RUNC-47; GABA;
KW   central nervous system disorder; peripheral nervous system disorder;
KW   neuropsychiatric; neuronal deficiency; gamma-aminobutyric acid; sedative;
KW   anxiolytic; transmembrane domain.
XX
OS   Rattus sp.
XX
PN   WO9920645-A1.
XX
PD   29-APR-1999.
XX
PF   23-OCT-1998;   98WO-US022587.
XX
PR   23-OCT-1997;   97US-0063012P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Edwards RH,  Reimer RJ,  Mcintire SL,  Jorgenson EM,  Schuske K;
XX
DR   WPI; 1999-302716/25.
XX
PT   Vesicular transporter protein useful for treating disorders of the
PT   central and/or peripheral nervous system.
XX
PS   Claim 3; Fig 1A-B; 52pp; English.
XX
CC   The invention relates to an amino acid synaptic vesicle transporter
CC   protein, UNC-47 and its rat homolog, RUNC-47. The vesicle transporter
CC   proteins can be used to identify candidate compounds that modulate amino
CC   acid transport into synaptic vesicles, these may be useful for treating
CC   disorders of the central and/or peripheral nervous system. RUNC-47 can be
CC   used to treat a subject having a neuropsychiatric condition characterised
CC   by neuronal deficiency of GABA (gamma-aminobutyric acid). Modulators of
CC   the proteins may also be useful for enhancing GABA uptake, which may
CC   produce sedative or anxiolytic effects. Sequences AAY17912-921 represent
CC   the transmembrane domains of the rat vesicular GABA transporter, RUNC-47
XX
SQ   Sequence 21 AA;

  Query Match             36.3%;  Score 33;  DB 2;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GTFALVSYI 13
              | ||||:|:
Db         11 GLFALVAYL 19
```

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AAR61467
ID   AAR61467 standard; peptide; 15 AA.
XX
AC   AAR61467;
XX
DT   16-SEP-1995  (first entry)
XX
DE   [Phe- or D-Phe-14] melittin-(7-21) analogue.
XX
KW   Peptide solid phase synthesis; polystyrene-grafted substrate; melittin.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 8
FT                   /note= "Phe or D-Phe"
XX
PN   US5373053-A.
XX
PD   13-DEC-1994.
XX
PF   14-DEC-1992;   92US-00990584.
XX
PR   01-SEP-1988;   88US-00239525.
PR   25-AUG-1989;   89US-00398846.
PR   12-MAY-1992;   92US-00882059.
XX
PA   (RISO-) RISO NAT LAB.
XX
PI   Berg RH,  Holm A,  Tam JP,  Pedersen WB,  Merrifield RB,  Almdal K;
XX
DR   WPI; 1995-030351/04.
XX
PT   substrate grafted with polystyrene - used in peptide synthesis giving
PT   high yields.
XX
PS   Example 9; Fig 3; 20pp; English.
XX
CC   The invention relates to a solid phase peptide synthesis method using a
CC   support consisting of a functionalised polystyrene-grafted polymer
CC   substrate. The peptides are prepared in high yield and purity. The
CC   process may be used for compartmentalised synthesis of a number of
CC   different peptides in parallel. The present sequence is one of 13
CC   melittin-(7-21) analogues prepared in parallel by the process (AAR61460-
CC   R61470)
XX
SQ   Sequence 15 AA;

  Query Match             35.2%;  Score 32;  DB 2;  Length 15;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GTFALVSYI 13
              | |||:|:|
Db          6 GLFALISWI 14
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AAR13129
ID   AAR13129 standard; protein; 15 AA.
XX
AC   AAR13129;
XX
DT   25-MAR-2003  (revised)
DT   01-OCT-1991  (first entry)
XX
DE   GPIb alpha peptide fragment.
XX
KW   Von Willebrand factor; vWF; platelet membrane glycoprotein Ib;
KW   glycoalicin; thrombosis.
XX
OS   Synthetic.
XX
PN   WO9109614-A.
XX
PD   11-JUL-1991.
XX
PF   04-JAN-1990;   90US-00460674.
XX
PR   04-JAN-1990;   90US-00460674.
PR   14-NOV-1990;   90US-00613083.
XX
PA   (SCRI ) SCRIPPS CLINIC & RES FOUND.
XX
PI   Ruggeri ZM,  Zimmerman TS,  Houghten RA,  Vicente V,  Mohri H;
PI   Ware JL;
XX
DR   WPI; 1991-222654/30.
XX
PT   GPIb alpha peptide fragment - inhibits binding of von Willebrand factor
PT   to platelet membrane glyco-protein Ib, useful in treating thrombosis.
XX
PS   Claim 1; Page 56; 76pp; English.
XX
CC   The peptide corresponds to residues 71-85 of the N-terminus of
CC   glycoalicin, a water sol. proteolytic fragment of GPIb alpha. It may be
CC   linked to a second peptide from the 45 kD N-terminal tryptic fragment of
CC   GPIb alpha. The peptide inhibits binding of vWF to GPIb. It can be used
CC   to inhibit activation, aggregation and/or adhesion of platelets, esp. for
CC   inhibition of thrombosis. See also AAR13128-R13138. (Updated on 25-MAR-
CC   2003 to correct PA field.)
XX
SQ   Sequence 15 AA;

  Query Match             33.0%;  Score 30;  DB 2;  Length 15;
  Best Local Similarity   66.7%;  Pred. No. 3.1e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 IPVLGTFAL 9
              :|||||  |
Db          6 LPVLGTLDL 14
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ADS13418
ID   ADS13418 standard; peptide; 17 AA.
XX
AC   ADS13418;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human rheumatoid arthritis marker peptide - SEQ ID 209.
XX
KW   rheumatoid arthritis; marker; antiinflammtory; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   WO2004082617-A2.
XX
PD   30-SEP-2004.
XX
PF   15-MAR-2004; 2004WO-US007880.
XX
PR   14-MAR-2003; 2003US-0455037P.
XX
PA   (SURR-) SURROMED INC.
XX
PI   Kantor AB,  Becker CH,  Schulman H;
XX
DR   WPI; 2004-690929/67.
XX
PT   New isolated marker for rheumatoid arthritis, useful in preparing a
PT   composition for diagnosing or treating rheumatoid arthritis.
XX
PS   Claim 1; SEQ ID NO 209; 184pp; English.
XX
CC   The invention relates to a novel isolated marker for rheumatoid arthritis
CC   selected from one of many (around 400) markers defined in the
CC   specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC   the small joints which is estimated to affect 2.1 million people in the
CC   United States alone. Current approaches to treat the disease include the
CC   use of non-steroidal antiinflammtory drugs (NSAIDS), which may reduce
CC   pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC   drugs (DMARDS), which act to slow the progression of the disease and
CC   avoid further joint injury. These drugs are associated with a number of
CC   serious side effects and the search for improved therapeutics is a
CC   subject of active research. The marker of the invention demonstrates
CC   antiarthritic activity and may be useful in preparing a composition for
CC   diagnosing or treating rheumatoid arthritis. The current sequence is that
CC   of a human rheumatoid arthritis marker peptide of the invention.
XX
SQ   Sequence 17 AA;

  Query Match             33.0%;  Score 30;  DB 8;  Length 17;
  Best Local Similarity   85.7%;  Pred. No. 3.6e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FALVSYI 13
              ||||:||
Db          8 FALVNYI 14
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